STIC Search Report
Biotech-Chem Library

TO: Rita Mitra
Location: REM-3B65
Art Unit: 1653
Monday, March 15, 2004

_234_

Case Serial Number: 09/976740

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Mitra,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

Look for WO ref.
& Pat. litem.
NPL ordered.

STIC Search Report
Biotech-Chem Library

Scientific & Technical Information Center
S T I C
USPTO

TO: Rita Mitra
Location: REM/3B65
Art Unit: 1653
Monday, March 15, 2004

3C70
234

Case Serial Number: 09/976740

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen E01A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

RUSH

Not elected
7, 17, 20, 21, 22

sira
Search and Information
Resources Administration

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 20:46:42 ; Search time 37.6157 Seconds
(without alignments)
2544.725 Million cell updates/sec

Title: US-09-976-740-20
Perfect score: 136
Sequence: 1 EEEDEDEDEDEDDVSEGSEVPESD 26

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19588/app_query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09976740 @CGN_1_712 @runat_10032004_094549_19588
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	136	100.0	78	9	US-09-962-055-31	Sequence 31, Appl
2	136	100.0	78	9	US-09-976-740-31	Sequence 31, Appl
3	136	100.0	78	12	US-10-671-242-31	Sequence 31, Appl
4	136	100.0	78	13	US-10-023-529-31	Sequence 31, Appl
5	136	100.0	78	15	US-10-023-523-31	Sequence 31, Appl
6	136	100.0	78	15	US-10-616-187-31	Sequence 31, Appl
7	136	100.0	78	15	US-10-616-187-31	Sequence 31, Appl
8	136	100.0	1208	9	US-09-962-055-16	Sequence 16, Appl
9	136	100.0	1208	12	US-09-976-740-16	Sequence 16, Appl
10	136	100.0	1208	13	US-10-023-523-16	Sequence 16, Appl
11	136	100.0	1208	15	US-10-616-187-16	Sequence 16, Appl
12	136	100.0	1336	14	US-10-806-247	Sequence 247, App
13	136	100.0	1614	13	US-09-945-527-6	Sequence 45, Appl
14	136	100.0	1614	14	US-09-976-740-45	Sequence 45, Appl
15	136	100.0	1445	10	US-09-976-740-45	Sequence 45, Appl
16	136	100.0	1614	13	US-10-671-242-45	Sequence 45, Appl
17	136	100.0	1614	13	US-10-023-529-45	Sequence 45, Appl
18	136	100.0	1614	15	US-10-023-523-45	Sequence 45, Appl
19	136	100.0	1614	13	US-10-616-187-45	Sequence 45, Appl
20	136	100.0	12425	12	US-09-976-740-50	Sequence 50, Appl
21	136	100.0	12425	12	US-10-671-242-50	Sequence 50, Appl
22	136	100.0	12425	13	US-10-023-529-50	Sequence 50, Appl
23	136	100.0	12425	15	US-10-023-523-50	Sequence 50, Appl
24	136	100.0	12425	15	US-10-616-187-50	Sequence 50, Appl
25	136	100.0	12425	13	US-09-962-055-37	Sequence 37, Appl
26	104.5	76.8	84	9	US-09-976-740-37	Sequence 37, Appl
27	104.5	76.8	84	13	US-10-671-242-37	Sequence 37, Appl
28	104.5	76.8	84	13	US-10-023-529-37	Sequence 37, Appl
29	104.5	76.8	84	15	US-10-023-523-37	Sequence 37, Appl
30	104.5	76.8	84	15	US-10-616-187-37	Sequence 37, Appl
31	104.5	76.8	1362	9	US-09-962-055-12	Sequence 12, Appl
32	104.5	76.8	1362	12	US-09-976-740-12	Sequence 12, Appl
33	104.5	76.8	1362	13	US-10-671-242-12	Sequence 12, Appl
34	104.5	76.8	1362	12	US-10-023-529-12	Sequence 12, Appl
35	104.5	76.8	1362	13	US-10-023-523-12	Sequence 12, Appl
36	104.5	76.8	1422	9	US-10-616-187-12	Sequence 12, Appl
37	104.5	76.8	1422	12	US-09-962-055-13	Sequence 13, Appl
38	104.5	76.8	1422	9	US-09-976-740-13	Sequence 13, Appl
39	104.5	76.8	1422	12	US-10-671-242-13	Sequence 13, Appl
40	104.5	76.8	1422	13	US-10-023-529-13	Sequence 13, Appl
41	104.5	76.8	1422	13	US-10-023-523-13	Sequence 13, Appl
42	104.5	76.8	1422	15	US-10-616-187-13	Sequence 13, Appl
43	104.5	76.8	1617	9	US-09-962-055-11	Sequence 11, Appl
44	104.5	76.8	1617	12	US-09-976-740-11	Sequence 11, Appl
45	104.5	76.8	1617	12	US-10-671-242-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-962-055-31
Sequence 31, Application US/09962055
Patent No. US2002005203341

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

```
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/962,055
  FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/979,608
  FILING DATE: 26-NOV-1997
  APPLICATION NUMBER: US 60/031,930
  FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Myers, Louis
  REGISTRATION NUMBER: 35,965
  REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 78 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..78
    SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-962-055-31

Alignment Scores:
Pred. No.:             1e-12
Score:                 136.00       Length:        78
Percent Similarity:    100.00%      Matches:       26
Best Local Similarity: 100.00%      Conservative:   0
Query Match:           100.00%      Mismatches:     0
DB:                    9            Indels:         0
                                    Gaps:           0

US-09-976-740-20 (1-26) x US-09-962-055-31 (1-78)

Qy   1  GluGluGluGluAspAspAspGluAspPGluAspPGluGluAspPGluGlyGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAAGATGGGTCT     60

Qy  21  GluValProGluSerAsp  26
        ||||||||||||||||||
Db  61  GAAGTGCCCGAGAGTGAC  78

RESULT 2
US-09-976-740-31
Sequence 31, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
  TITLE OF INVENTION: ATHEROSCLEROSIS
  FILE REFERENCE: 1079-004001
  CURRENT APPLICATION NUMBER: US/09/976,740
  CURRENT FILING DATE: 2001-10-12
  PRIOR APPLICATION NUMBER: 09/616,289
  PRIOR FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: US 60/031,930
  PRIOR FILING DATE: 1996-11-27
  PRIOR APPLICATION NUMBER: US 60/048,547
  PRIOR FILING DATE: 1997-06-03
  PRIOR APPLICATION NUMBER: US 08/979,608
  PRIOR FILING DATE: 1997-11-26
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 31
  LENGTH: 78
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-976-740-31

US-09-976-740-20 (1-26) x US-09-976-740-31 (1-78)

Qy   1  GluGluGluGluAspAspAspGluAspPGluAspPGluGluAspPGluGlyGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAAGATGGGCTCT    60

Qy  21  GluValProGluSerAsp  26
        ||||||||||||||||||
Db  61  GAAGTGCCCGAGAGTGAC  78

RESULT 3
US-10-671-242-31
Sequence 31, Application US/10671242
Publication No. US20040040045A1
GENERAL INFORMATION:
  APPLICANT: Lees, Robert S.
  APPLICANT: Lees, Ann M.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
  TITLE OF INVENTION: ATHEROSCLEROSIS
  FILE REFERENCE: 10797-004001
  CURRENT APPLICATION NUMBER: US/10/671,242
  CURRENT FILING DATE: 2003-09-24
  PRIOR APPLICATION NUMBER: US/09/616,289
  PRIOR FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: US 09/517,849
  PRIOR FILING DATE: 2000-03-02
  PRIOR APPLICATION NUMBER: US 08/979,608
  PRIOR FILING DATE: 1997-11-26
  PRIOR APPLICATION NUMBER: US 60/031,930
  PRIOR FILING DATE: 1996-11-27
  PRIOR APPLICATION NUMBER: US 60/048,547
  PRIOR FILING DATE: 1997-06-03
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 31
  LENGTH: 78
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-671-242-31

Alignment Scores:
Pred. No.:             1e-12
Score:                 136.00       Length:        78
Percent Similarity:    100.00%      Matches:       26
Best Local Similarity: 100.00%      Conservative:   0
Query Match:           100.00%      Mismatches:     0
DB:                    12           Indels:         0
                                    Gaps:           0

US-09-976-740-20 (1-26) x US-10-671-242-31 (1-78)

Qy   1  GluGluGluGluAspAspAspGluAspPGluAspPGluGluAspPGluGlyGlySer  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAAGATGGGCTCT    60

Qy  21  GluValProGluSerAsp  26
        ||||||||||||||||||
Db  61  GAAGTGCCCGAGAGTGAC  78
```

RESULT 4
US-10-023-529-31
Sequence 31, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-31

Alignment Scores:
Pred. No.:   1e-12   Length: 78
Score: 136.00   Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 13   Gaps: 0

US-09-976-740-20 (1-26) x US-10-023-529-31 (1-78)

```
Qy  1 GluGluGluGluAspAspAspGluAspGluGluAspPValSerGluGlySer 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 GAAGAGGAAGAAGATCATGATGATGAACGATGAAGAAGATGAAGAAGATGATGTGTCAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 5
US-10-023-523-31
Sequence 31, Application US/10023523
Publication No. US20020152485A1
GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-523-31

Alignment Scores:
Pred. No.:   1e-12   Length: 78
Score: 136.00   Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 13   Gaps: 0

US-09-976-740-20 (1-26) x US-10-023-523-31 (1-78)

```
Qy  1 GluGluGluGluAspAspAspGluAspGluGluAspPValSerGluGlySer 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 GAAGAGGAAGAAGATCATGATGATGAACGATGAAGAAGATGAAGAAGATGATGTGTCAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 6
US-10-616-187-31
Sequence 31, Application US/10616187
Publication No. US20040013668A1
GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-187-31

Alignment Scores:
Pred. No.:   1e-12   Length: 78
Score: 136.00   Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 15   Gaps: 0

US-09-976-740-20 (1-26) x US-10-616-187-31 (1-78)

```
Qy  1 GluGluGluGluAspAspAspGluAspGluGluAspPValSerGluGlySer 20
```

Db 1 GAAGGAGGAAGAAGATGATGAAGAAGAAGAAGATGATGTGTCAGAGGGCTCT 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 21 GluValProGluSerAsp 26

Qy 61 GAAGTGCCCGAGAGTGAC 78
       ||||||||||||||||||
Db

RESULT 7
US-09-962-055-16
; Sequence 16, Application US/09962055
; Patent No. US2002052033A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/962,055
;   FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/979,608
;   FILING DATE: 26-NOV-1997
;   APPLICATION NUMBER: US 60/031,930
;   FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..651
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-962-055-16

Alignment Scores:
Pred. No.:
Score: 1.52e-11
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9

Length: 1208
Matches: 26
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-20 (1-26) x US-09-962-055-16 (1-1208)

Qy 1 GluGluValProGluSerAspAlaSpGluAspGluAspGluAspAspValSerGluGlySer 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAAGATGATGAAGAAGAAGAAGATGATGTGTCAGAGGGCTCT 81

Qy 21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db 82 GAAGTGCCCGAGAGTGAC 99

RESULT 8
US-09-976-740-16
; Sequence 16, Application US/09976740
; Publication No. US2002019463A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(651)
US-09-976-740-16

Alignment Scores:
Pred. No.:
Score: 1.52e-11
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9

Length: 1208
Matches: 26
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-20 (1-26) x US-09-976-740-16 (1-1208)

Qy 1 GluGluValProGluSerAsp 26
       |||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAAGATGATGAAGAAGAAGAAGATGATGTGTCAGAGGGCTCT 81

Qy 21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db 82 GAAGTGCCCGAGAGTGAC 99

RESULT 9
US-10-671-242-16
; Sequence 16, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14

```
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 16
;  LENGTH: 1208
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(651)
US-10-671-242-16

Alignment Scores:
Pred. No.:               1.52e-11      Length:          1208
Score:                   136.00        Matches:         26
Percent Similarity:      100.00%       Conservative:    0
Best Local Similarity:   100.00%       Mismatches:      0
Query Match:             12            Indels:          0
DB:                                    Gaps:            0

US-09-976-740-20 (1-26) x US-10-671-242-16 (1-1208)

Qy    1  GluGluGluAspAspAspGluAspGlyGluGluAspAspValSerGluGlySer  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22  GAAGAGGAAGGAAGATGATGATGAAGATGATGAAGAAGATGATGTGTCAGAGGGGCTCT  81

Qy   21  GluValProGluSerAsp  26
         ||||||||||||||||||
Db   82  GAAGTGCCCGAGAGTGAC  99

RESULT 10
US-10-023-529-16
; Sequence 16, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 16
;  LENGTH: 1208
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(651)
US-10-023-529-16

Alignment Scores:
Pred. No.:               1.52e-11      Length:          1208
Score:                   136.00        Matches:         26
Percent Similarity:      100.00%       Conservative:    0
Best Local Similarity:   100.00%       Mismatches:      0
Query Match:             13            Indels:          0
DB:                                    Gaps:            0

US-09-976-740-20 (1-26) x US-10-023-529-16 (1-1208)

Qy    1  GluGluGluAspAspAspGluAspGlyGluGluAspAspValSerGluGlySer  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22  GAAGAGGAAGGAAGATGATGATGAAGATGATGAAGAAGATGATGTGTCAGAGGGGCTCT  81

Qy   21  GluValProGluSerAsp  26
         ||||||||||||||||||
Db   82  GAAGTGCCCGAGAGTGAC  99

RESULT 11
US-10-023-523-16
; Sequence 16, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,523
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 16
;  LENGTH: 1208
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(651)
US-10-023-523-16

Alignment Scores:
Pred. No.:               1.52e-11      Length:          1208
Score:                   136.00        Matches:         26
Percent Similarity:      100.00%       Conservative:    0
Best Local Similarity:   100.00%       Mismatches:      0
Query Match:             13            Indels:          0
DB:                                    Gaps:            0

US-09-976-740-20 (1-26) x US-10-023-523-16 (1-1208)

Qy    1  GluGluGluAspAspAspGluAspGlyGluGluAspAspValSerGluGlySer  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22  GAAGAGGAAGGAAGATGATGATGAAGATGATGAAGAAGATGATGTGTCAGAGGGGCTCT  81

Qy   21  GluValProGluSerAsp  26
         ||||||||||||||||||
Db   82  GAAGTGCCCGAGAGTGAC  99

RESULT 12
```

US-10-616-187-16
; Sequence 16, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: ATHROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-05-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-616-187-16

Alignment Scores:
Pred. No.:
Score: 1.52e-11
Percent Similarity: 136.00
Best Local Similarity: 100.00%
Query Match: 100.00%
                            15

                            Length: 1208
                            Matches: 26
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

US-09-976-740-20 (1-26) x US-10-616-187-16 (1-1208)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAspAspValSerGluGlySer 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAGAAGAAGATGAATGAAGATGAAGAAGAAGATGAATGTGTCAGAGGGCTCT 81

US-10-102-806-247
; Sequence 247, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 247
; LENGTH: 1336

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1336)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-247

Alignment Scores:
Pred. No.:
Score: 1.68e-11
Percent Similarity: 136.00
Best Local Similarity: 100.00%
Query Match: 100.00%
                            14

                            Length: 1336
                            Matches: 26
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

US-09-976-740-20 (1-26) x US-10-102-806-247 (1-1336)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAspAspValSerGluGlySer 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 GAAGAGGAGAAGAAGATGAATGAAGATGAAGAAGAAGATGAATGTGTCAGAGGGCTCT 171

RESULT 14
US-09-945-527-6
; Sequence 6, Application US/09945527
; Publication No. US20030055588A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20030055588Alel Nucleic Acid Molecules Encoding
; TITLE OF INVENTION: Nucleic Acid and Protein Homologs
; FILE REFERENCE: 35800/237985
; CURRENT APPLICATION NUMBER: US/09/945,527
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-945-527-6

Alignment Scores:
Pred. No.:
Score: 1.82e-11
Percent Similarity: 136.00
Best Local Similarity: 100.00%
Query Match: 100.00%
                            10

                            Length: 1445
                            Matches: 26
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

US-09-976-740-20 (1-26) x US-09-945-527-6 (1-1445)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAspAspValSerGluGlySer 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 GAAGAGGAGAAGAAGATGAATGAAGATGAAGAAGAAGATGAATGTGTCAGAGGGCTCT 266

RESULT 15
US-09-976-740-45
; Sequence 45, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   154 GAAGTGCCCGAGAGTGAC 171

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   207 GAAGTGCCCGAGAGTGAC 266

RESULT 13
US-10-102-806-247

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   267 GAAGTGCCCGAGAGTGAC 284

```
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION:  NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/09/976,740
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE:  2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE:  1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE:  1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE:  1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;
;  SEQ ID NO 45
;  LENGTH: 1614
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(1614)
US-09-976-740-45

Alignment Scores:
Pred. No.:               2.03e-11      Length:         1614
Score:                   136.00        Matches:        26
Percent Similarity:      100.00%       Conservative:   0
Best Local Similarity:   100.00%       Mismatches:     0
Query Match:             100.00%       Indels:         0
DB:                      9             Gaps:           0

US-09-976-740-20 (1-26) x US-09-976-740-45 (1-1614)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspAspValSerGluGlySer  20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985 GAAGAGGAGGAAGAATGATGATGAAGATGAAGATGAAGAAGATGATGTGTCAGAGGGCTCT 1044

Qy     21 GluValProGluSerAsp  26
          ||||||||||||||||||
Db   1045 GAAGTGCCCGAGAGTGAC 1062

Search completed: March 13, 2004,  04:26:14
Job time : 38.6157 secs
```

OM protein - nucleic search, using frame_plus_p2n model

```
                              GenCore version 5.1.6
                        Copyright (c) 1993 - 2004 Compugen Ltd.
```

Run on: March 12, 2004, 19:55:37 ; Search time 393.119 Seconds
                                     (without alignments)
                                     1975.018 Million cell updates/sec

Title: US-09-976-740-20
Perfect score: 136
Sequence: 1 EEEEDDDEDDEDDVSEGSEVPESD 26

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop   6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 27513289 seqs, 1493109027б residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model   -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat 10032004 094548_19551/app_query.fasta_1.1898
-DB=EST -QFMT=fastap -SUFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US09976740 @CGN 1 1 10212 @runat 10032004 094548_19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120. -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
  EST.*
   1:   em_estba:*
   2:   em_esthum:*
   3:   em_estin:*
   4:   em_estmu:*
   5:   em_estvrt:*
   6:   em_estov:*
   7:   em_estpl:*
   8:   em_estro:*
   9:   em_htc:*
  10:   em_est1:*
  11:   gb_est2:*
  12:   gb_htc:*
  13:   gb_est3:*
  14:   gb_est4:*
  15:   gb_est5:*
  16:   em_estfun:*
  17:   em_estom:*
  18:   em_gss_hum:*
  19:   em_gss_inv:*
  20:   em_gss_pln:*
  21:   em_gss_vrt:*
  22:   em_gss_fun:*
  23:   em_gss_nam:*
  24:   em_gss_mus:*
  25:   em_gss_pro:*
  26:   em_gss_rod:*
  27:   em_gss_phg:*
  28:   gb_gssl:*
  28:   gb_gssl:*
```

29: gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 136 | 100.0 | 271 | 9 | AA765474 | AA765474 oa03d01.s |
| 2 | 136 | 100.0 | 274 | 12 | BI004562 | BI004562 MR4-HN005 |
| C | 3 | 136 | 100.0 | 275 | 9 | AA806888 | AA806888 oc32g06.s |
| 4 | 136 | 100.0 | 278 | 9 | AA810871 | AA810871 ob64g05.s |
| 5 | 136 | 100.0 | 284 | 9 | AA766034 | AA766034 oa15b09.s |
| 6 | 136 | 100.0 | 302 | 10 | BF194967 | BF194967 7o91b05.x |
| 7 | 136 | 100.0 | 322 | 9 | AI470106 | AI470106 tj90g09.x |
| 8 | 136 | 100.0 | 324 | 10 | BF806978 | BF806978 Qv4-CT015 |
| 9 | 136 | 100.0 | 345 | 10 | BF941758 | BF941758 nad92h03. |
| 10 | 136 | 100.0 | 367 | 9 | AA769505 | AA769505 n235b01.s |
| 11 | 136 | 100.0 | 383 | 10 | AW845391 | AW845391 CM4-CT004 |
| 12 | 136 | 100.0 | 384 | 11 | AA836383 | AA836383 od37b07.s |
| 13 | 136 | 100.0 | 397 | 10 | AW594381 | AW594381 hg68e08.x |
| 14 | 136 | 100.0 | 412 | 10 | AW134620 | AW134620 UI-H-BI1- |
| 15 | 136 | 100.0 | 429 | 9 | AI379283 | AI379283 qb87g10.x |
| 16 | 136 | 100.0 | 446 | 9 | AW016794 | AW016794 tc73b06.x |
| 17 | 136 | 100.0 | 451 | 9 | AI186973 | AI186973 qe28f06.x |
| 18 | 136 | 100.0 | 455 | 9 | AW054879 | AW054879 ws96a12.x |
| 19 | 136 | 100.0 | 460 | 9 | AI921818 | AI921818 wn65f06.x |
| 20 | 136 | 100.0 | 461 | 10 | BF061129 | BF061129 7i81c12.x |
| 21 | 136 | 100.0 | 466 | 9 | AI819090 | AI819090 wj60h05.x |
| 22 | 136 | 100.0 | 467 | 9 | AI961519 | AI961519 wt23g10.x |
| 23 | 136 | 100.0 | 472 | 9 | AI888659 | AI888659 wk29e03.x |
| 24 | 136 | 100.0 | 480 | 9 | AI569682 | AI569682 tn04d11.x |
| 25 | 136 | 100.0 | 483 | 9 | AI186705 | AI186705 qe82e05.x |
| 26 | 136 | 100.0 | 487 | 9 | AI186705 | AI186705 qe82e05.x |
| 27 | 136 | 100.0 | 495 | 9 | AI199022 | AI199022 qi39g04.x |
| 28 | 136 | 100.0 | 501 | 9 | AI796089 | AI796089 wh42c02.x |
| 29 | 136 | 100.0 | 509 | 9 | AI632586 | AI632586 wb10g11.x |
| 30 | 136 | 100.0 | 512 | 10 | AW15766 | AW15766 hd8Bb04.x |
| 31 | 136 | 100.0 | 518 | 10 | BE269536 | BE269536 601B4757 |
| 32 | 136 | 100.0 | 572 | 12 | BM697252 | BM697252 UI-E-DX0- |
| 33 | 136 | 100.0 | 580 | 10 | BE257093 | BE257093 601108824 |
| 34 | 136 | 100.0 | 583 | 10 | AI660679 | AI660679 wf23e11.x |
| 35 | 136 | 100.0 | 590 | 9 | AI123580 | AI123580 qa50b10.x |
| 36 | 136 | 100.0 | 593 | 10 | AI928488 | AI928488 wp02e10.x |
| 37 | 136 | 100.0 | 680 | 10 | BE675122 | BE675122 7f02h07.x |
| 38 | 136 | 100.0 | 683 | 10 | BE857956 | BE857956 7f73a12.x |
| 39 | 136 | 100.0 | 686 | 10 | BE513784 | BE513784 601115608 |
| 40 | 136 | 100.0 | 704 | 10 | BF058975 | BF058975 7k36f08.x |
| 41 | 136 | 100.0 | 707 | 10 | BF469961 | BF469961 601580888 |
| 42 | 136 | 100.0 | 743 | 10 | BF058118 | BF058118 7k38e12.x |
| 43 | 136 | 100.0 | 774 | 10 | BE891267 | BE891267 601432095 |
| 44 | 136 | 100.0 | 785 | 12 | BI226646 | BI226646 602951660 |
| 45 | 136 | 100.0 | 828 | 10 | BE794500 | BE794500 601590248 |

ALIGNMENTS

```
RESULT 1
AA765474
LOCUS        AA765474          271 bp    mRNA    linear    EST 08-FEB-1998
DEFINITION   oa03d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303873 3'
             similar to contains Alu repetitive element;contains element MER22
             repetitive element i, mRNA sequence.
ACCESSION    AA765474
VERSION      AA765474.1    GI:2816712
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE   1 (bases 1 to 271)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
TITLE
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Insert Length: 1136   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 269.
FEATURES   Location/Qualifiers
     source   1..271
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1303873"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGGCGGCCGCCCCTTTTTTTTTTTTTTTT-3',
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x AA765474 (1-271)

Alignment Scores:
Pred. No.:
Score: 1.61e-07   Length: 271
                                       Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Percent Identity: 100.00%   Mismatches: 0
Best Local Similarity: 100.00%   Indels: 0
Query Match: 9   Gaps: 0
DB:

Qy   1 GluGluGluGluAspAlaAspGluAspGluGluAspAspValSerGluGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 GAAGAGGAGAAGAAGATGATGAAGATGAAGAGAGATGAGGAAGAGATGAGTGTCAGAGGGCTCT 141

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 142 GAAGTGCCCGAGAGTGAC 159

RESULT 2
LOCUS   BI004562/c   274 bp   mRNA   linear   EST 13-JUN-2001
DEFINITION MR4-HN0054-070301-002-g04 HN0054 Homo sapiens cDNA clone, mRNA sequence.
ACCESSION   BI004562
VERSION   BI004562.1 GI:1408636
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 274)

AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
             O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20226663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR4&t2=MR4-HN0054-
             070301-002-g04t3=2001-03-07&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 39
             High quality sequence stop: 274.
FEATURES   Location/Qualifiers
     source   1..274
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="HN0054"
                     /dev_stage="Adult"
                     /note="Organ: head.normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

US-09-976-740-20 (1-26) x BI004562 (1-274)

Alignment Scores:
Pred. No.:
Score: 1.63e-07   Length: 274
                                       Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Percent Identity: 100.00%   Mismatches: 0
Best Local Similarity: 100.00%   Indels: 0
Query Match: 12   Gaps: 0
DB:

Qy   1 GluGluGluGluAspAlaAspGluAspGluGluAspAspValSerGluGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 251 GAAGAGGAGAAGAAGATGATGAAGATGAAGAGAGATGAGGAAGAGATGAGTGTCAGAGGGCTCT 192

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 191 GAAGTGCCCGAGAGTGAC 174

RESULT 3
LOCUS   AA806888   275 bp   mRNA   linear   EST 07-APR-1998
DEFINITION oc32g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351450 3',
            similar to contains element TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AA806888
VERSION   AA806888.1 GI:2876464
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 275)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE   Tumor Gene Index
            Unpublished (1997)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1112   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 229.
FEATURES   Location/Qualifiers
     source   1..275
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1351450"
                     /tissue_type="germinal center B cell"
                     /clone_lib="NCI_CGAP_GCB1"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGACGCGGCCGCCCTCATTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x AA806888 (1-275)

Alignment Scores:
Pred. No.:   1.63e-07
Score: 136.00   Length: 275
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 9   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluAspAspAspGluAspGlyGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85 GAAGAGGAAGAGGATGATGATGAAGATGATGAAGAAGATGATGTGTCAGAGGGCTCT 144

Qy   21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 145 GAAGTGCCCGAGAGTGAC 162

RESULT 4
LOCUS   AA810871   278 bp   mRNA   linear   EST 19-FEB-1998
DEFINITION ob64g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336184 3'
            similar to contains element PTR7 repetitive element ;, mRNA
            sequence.
ACCESSION   AA810871
VERSION   AA810871.1   GI:2880482
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE   1 (bases 1 to 278)
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE   Tumor Gene Index
            Unpublished (1997)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1143   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 269.
FEATURES   Location/Qualifiers
     source   1..278
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1336184"
                     /tissue_type="germinal center B cell"
                     /clone_lib="NCI_CGAP_GCB1"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGACGCGGCCGCCCTCATTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x AA810871 (1-278)

Alignment Scores:
Pred. No.:   1.65e-07
Score: 136.00   Length: 278
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 9   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluAspAspAspGluAspGlyGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 GAAGAGGAAGAGGATGATGATGAAGATGATGAAGAAGATGATGTGTCAGAGGGCTCT 141

Qy   21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 142 GAAGTGCCCGAGAGTGAC 159

RESULT 5
LOCUS   AA766034   284 bp   mRNA   linear   EST 08-FEB-1998
DEFINITION oa1sb09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:130501? 3'
            similar to contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   AA766034
VERSION   AA766034.1   GI:2817272
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 284)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1100   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1..284
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1305017"
                     /tissue_type="germinal center B cell"
                     /clone_lib="NCI_CGAP_GCB1"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGGGGCGCGCCCTCATTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x AA766034 (1-284)

Alignment Scores:
Pred. No.:              1      1.69e-07
Score:                  136.00           Length:        284
Percent Similarity:     100.00%          Matches:       26
Best Local Similarity:  100.00%          Conservative:  0
Query Match:            9                Mismatches:    0
                                         Indels:        0
                                         Gaps:          0

Qy    1  GluGluGluGluAspAspGluAspGluGluAspAspAspValSerGluGluGlySer  20
         |||||||||||||||||||||||
Db   81  GAAGAGGAAGAAGAATGATGATGAAGAAGATGAAGAAGATGATGTTCAGAGAGGGCTCT  140

Qy   21  GluValProGluSerAsp  26
         ||||||||||||||||||
Db  141  GAAGTGCCCGAGAGTGAC  158

RESULT 6
LOCUS       BF194967        302 bp    mRNA    linear   EST 03-NOV-2000
DEFINITION  7o91b05.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643712 3'
            similar to contains element TAR1 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   BF194967
VERSION     BF194967.1  GI:11081346
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 302)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium
            DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov.
FEATURES             Location/Qualifiers
     source          1..302
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3643712"
                     /tissue_type="fibrotheoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NCI_CGAP_Ov18"
                     /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'-
                     TGTTACCAATCTGAAGTGGGAGGGGCGCGCCGCCGACATTTTTTTTTTTTTTTTT-3'];
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x BF194967 (1-302)

Alignment Scores:
Pred. No.:              1      1.82e-07
Score:                  136.00           Length:        302
Percent Similarity:     100.00%          Matches:       26
Best Local Similarity:  100.00%          Conservative:  0
Query Match:            10               Mismatches:    0
                                         Indels:        0
                                         Gaps:          0

Qy    1  GluGluGluGluAspAspGluAspGluGluAspAspAspValSerGluGluGlySer  20
         |||||||||||||||||||||||
Db  168  GAAGAGGAAGAAGAATGATGATGAAGAAGATGAAGAAGATGATGTTCAGAGAGGGCTCT  227

Qy   21  GluValProGluSerAsp  26
         ||||||||||||||||||
Db  228  GAAGTGCCCGAGAGTGAC  245

RESULT 7
AI470106
LOCUS       AI470106        322 bp    mRNA    linear   EST 14-APR-1999
DEFINITION  tj9cg09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2148832 3' similar to contains TAR1.b2 PTR5 repetitive
            element ;, mRNA sequence.
ACCESSION   AI470106
VERSION     AI470106.1  GI:4332196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 322)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
```

JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.lnl.gov) for further information.
           Insert Length: 387   Std Error: 0.00
           Seq primer: -40UP from Gibco.
FEATURES   Location/Qualifiers
     source   1..322
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2148832"
                      /clone_lib="Soares NSF_F8_9W_OT_PA_P_S1"
                      /lab_host="DH10B"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site 1: Not I; Site 2: Eco RI;
                      Equal amounts of plasmid DNA from five normalized
                      libraries were mixed, and ss circles were made in vitro.
                      Following HAP purification, this DNA was used as tracer in
                      a subtractive hybridization reaction. The driver was
                      PCR-amplified cDNAs from pools of 5,000 clones made from
                      the same 5 libraries. The pools consisted of the following
                      libraries and cloneIDs: Soares NbHSF pool 1:
                      303384-310919, 323208-325895 Soares Nb2HP pool 1:
                      14532-147335, 147720-148103, 148872-149255, 15002 -
                      150407, 151176-152327 Soares Nb2H8-9W pool 1:
                      752280-760583, 771104-774407 Soares NbHPA pool 1:
                      304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                      pool 1: 723720-726407, 739080-740999 Subtraction by Bento
                      Soares and M. Fatima Bonaldo."
ORIGIN

US-09-976-740-20 (1-26) x AI470106 (1-322)

Alignment Scores:
Pred. No.:   1.96e-07
Score: 136.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9
DB: 212

    Length: 322
    Matches: 26
    Conservative: 0
    Mismatches: 0
    Indels: 0
    Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluGluGluAspAspAspValSerGluGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 152 GAAGAGGAAGAAGAAGATGACATGACATGAAGAAGATGATGTGTCAGAGGGCTCT 211

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||||||
Db 212 GAAGTGCCCGAGAGTGAC 229

RESULT 8
BF806978
LOCUS   BF806978   324 bp   mRNA   linear   EST 12-JAN-2001
DEFINITION QV4-CIO151-091100-522-a05 CIO151 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF806978
VERSION   BF806978.1 GI:12135967
KEYWORDS   EST.
SOURCE   Homo sapiens
  ORGANISM Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 324)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663

PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4-CIO151-
           091100-522-a05&t3=2000-11-09&t4=1)
           Seq primer: Puc 18 forward
           Seq primer stop: 324.
           High quality sequence stop: 324.
FEATURES   Location/Qualifiers
     source   1..324
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="adult"
                      /clone="CIO151"
                      /clone_lib="CIO151"
                      /note="Organ: colon; Vector: puc18; Site 1: Smal;
                      Site 2: Smal; A mini-library was made by cloning products
                      derived from ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 - Ludwig Institute for Cancer Research)
                      profiles into the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
ORIGIN

US-09-976-740-20 (1-26) x BF806978 (1-324)

Alignment Scores:
Pred. No.:   1.97e-07
Score: 136.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 10
DB: 107

    Length: 324
    Matches: 26
    Conservative: 0
    Mismatches: 0
    Indels: 0
    Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluGluGluAspAspAspValSerGluGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47 GAAGAGGAAGAAGAAGATGACATGACATGAAGAAGATGATGTGTCAGAGGGCTCT 106

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||||||
Db 107 GAAGTGCCCGAGAGTGAC 124

RESULT 9
BF941758
LOCUS   BF941758   345 bp   mRNA   linear   EST 30-MAR-2001
DEFINITION nad92h03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3433564 3',
            similar to contains element PTR5 repetitive element ;, mRNA
            sequence.
ACCESSION   BF941758
VERSION   BF941758.1 GI:12359078
KEYWORDS   EST.
SOURCE   Homo sapiens
  ORGANISM Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D cDNA Library Preparation: M. Bento
            Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Left column

Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 325.

```
FEATURES          Location/Qualifiers
source            1..345
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3433564"
                  /tissue_type="fibrotheoma"
                  /clone_lib="NCI_CGAP_Ov18"
                  /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                  modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                  strand cDNA was primed with a Not I - oligo(dT) primer [5'
                  TGTTACCAATCTGAAGTGGGAGGAGGACGCGTGCCGCCGCCGCCGCCGCCATTTTTTTTTTTTTTTTTTT 3'];
                  double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Not I and cloned into the Not
                  I and Eco RI sites of the modified pT7T3 vector. Library
                  went through one round of normalization, and was
                  constructed by Bento Soares and M. Fatima Bonaldo.  "

ORIGIN
```

Alignment Scores:

Pred. No.:	2.12e-07
Score:	136.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	10

US-09-976-740-20 (1-26) x BF941758 (1-345)

```
Qy    1 GluGluGlu2luAspAspAspGluGluGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  159 GAAGAGGAAGAAGAATGAGAATGAAGAAGAAGAAGATGAAGAAGATGAAGAT 218

Qy   21 GluValProGluSerAsp 26
        ||||||||||||||||
Db  219 GAAGTGCCCGAGAGTGAC 236
```

RESULT 10
AA769505

```
LOCUS       AA769505        367 bp    mRNA    linear    EST 07-FEB-1998
DEFINITION  nz35b01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289737 3'
            similar to contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   AA769505
VERSION     AA769505.1  GI:2820743
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 367)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
```

Right column

Insert Length: 1136   Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 366.

```
FEATURES          Location/Qualifiers
source            1..367
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:1289737"
                  /tissue_type="germinal center B cell"
                  /clone_lib="NCI_CGAP_GCB1"
                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                  polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                  was prepared from human tonsillar cells enriched for
                  germinal center B cells by flow sorting (CD20+, IgD-),
                  provided by Dr. Louis M. Staudt (CBER). Dr. David Allman
                  (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                  primed with a Not I - oligo(dT) primer
                  [5'-TGTTACCAATCTGAAGTGGGAGGAGGACGCGTGCCGCCGCCATTTTTTTTTTTTTTTTTTTT-3'
                  ]. Double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Not I and cloned into the Not I
                  and Eco RI sites of the modified pT7T3 vector. Library
                  went through one round of normalization, and was
                  constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
```

Alignment Scores:

Pred. No.:	2.27e-07
Score:	136.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	9

US-09-976-740-20 (1-26) x AA769505 (1-367)

```
Qy    1 GluGluGlu2luAspAspAspGluGluGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  105 GAAGAGGAAGAAGAATGAGAATGAAGAAGAAGAAGATGAAGAAGATGAAGAT 164

Qy   21 GluValProGluSerAsp 26
        ||||||||||||||||
Db  165 GAAGTGCCCGAGAGTGAC 182
```

RESULT 11
AW845391

```
LOCUS       AW845391        383 bp    mRNA    linear    EST 19-MAY-2000
DEFINITION  CM4-CT0045-180200-512-h05 CT0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW845391
VERSION     AW845391.1  GI:7940908
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 383)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
```

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-CT0045-180
200-512-h05t3=2000-02-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 312.

FEATURES　　　　Location/Qualifiers
source　　　　1..383
　　　　/organism="Homo sapiens"
　　　　/mol_type="mRNA"
　　　　/db_xref="taxon:9606"
　　　　/dev_stage="Adult"
　　　　/clone_lib="CT0045"
　　　　/clone="CT0045-180"
　　　　/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2:
　　　　SmaI; A mini-library was made by cloning products derived
　　　　from ORESTES PCR (U.S. Letters Patent application No.
　　　　196,716. - Ludwig Institute for Cancer Research) profiles
　　　　into the pUC 18 vector. Reverse transcription of tissue
　　　　mRNA and cDNA amplification were performed under low
　　　　stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.:
Score:　　　　　　　2.39e-07
Percent Similarity:　136.00
Best Local Similarity:　100.00%
Query Match:　　　100.00%
DB:　　　　　　10

Length:　　383
Matches:　　26
Conservative:　0
Mismatches:　0
Indels:　　　0
Gaps:　　　0

US-09-976-740-20 (1-26) x AW845391 (1-383)

Qy　　1 GluGluGluGluAspAspAspGluAspGluGluGluAspAspAspValSerGluGlySer 20
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　139 GAAGAGGAAGAAGATCATGATGAAGAAGAAGATGAAGAAGAAGATGAAGTGTCAGAGGGCTCT 198

Qy　21 GluValProGluSerAsp 26
　　　　|||||||||||||||||
Db　199 GAAGTGCCCGAGAGTGAC 216

RESULT 12
LOCUS　　　　AA836383
AA836383
DEFINITION　od37b07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1370101
　　　　similar to contains element PTR7 repetitive element ;, mRNA
　　　　sequence.
ACCESSION　AA836383
VERSION　　AA836383.1　GI:2910702
KEYWORDS　EST.
SOURCE　　Homo sapiens (human)
ORGANISM　Homo sapiens
　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　1　(bases 1 to 384)
AUTHORS　NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE　　National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
　　　　Tumor Gene Index
JOURNAL　Unpublished (1997)
COMMENT　Contact: Robert Strausberg, Ph.D.
　　　　Email: cgapbs-r@mail.nih.gov
　　　　Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
　　　　Ph.D., Gerald Marti, M.D.
　　　　cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
　　　　Bonaldo, Ph.D.
　　　　cDNA Library Arrayed by: Greg Lennon, Ph.D.
　　　　DNA Sequencing by: Washington University Genome Sequencing Center
　　　　Clone distribution: NCI-CGAP clone distribution information can be
　　　　found through the I.M.A.G.E. Consortium/LLNL at:
　　　　www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 1153　Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 373.

FEATURES　　　　Location/Qualifiers
source　　　　1..384
　　　　/organism="Homo sapiens"
　　　　/mol_type="mRNA"
　　　　/db_xref="taxon:9606"
　　　　/clone="IMAGE:1370101"
　　　　/tissue_type="germinal center B cell"
　　　　/lab_host="DH10B"
　　　　/clone_lib="NCI_CGAP_GCB1"
　　　　/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
　　　　polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
　　　　was prepared from human tonsillar cells enriched for
　　　　germinal center B cells by flow sorting (CD20+, IgD-),
　　　　provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
　　　　(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
　　　　primed with a Not I - oligo(dT) primer
　　　　[5'-TGTTACCAATCTGAAGTGGGACGCGGCGCGCCGCCCATTTTTTTTTTTTTTT-3'
　　　　]. Double-stranded cDNA was ligated to Eco RI adaptors
　　　　(Pharmacia), digested with Not I and cloned into the Not I
　　　　and Eco RI sites of the modified pT7T3 vector. Library
　　　　went through one round of normalization, and was
　　　　constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:
Score:　　　　　　　2.39e-07
Percent Similarity:　136.00
Best Local Similarity:　100.00%
Query Match:　　　100.00%
DB:　　　　　　9

Length:　　384
Matches:　　26
Conservative:　0
Mismatches:　0
Indels:　　　0
Gaps:　　　0

US-09-976-740-20 (1-26) x AA836383 (1-384)

Qy　　1 GluGluGluGluAspAspAspGluAspGluGluGluAspAspAspValSerGluGlySer 20
　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　76 GAAGAGGAAGAAGATCATGATGAAGAAGAAGATGAAGAAGAAGATGAAGTGTCAGAGGGCTCT 135

Qy　21 GluValProGluSerAsp 26
　　　　|||||||||||||||||
Db　136 GAAGTGCCCGAGAGTGAC 153

RESULT 13
AW594381
LOCUS　　　　AW594381
DEFINITION　hg68e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2950790 3'
　　　　similar to contains PTR5.t1 PTR5 repetitive element ;, mRNA
　　　　sequence.
ACCESSION　AW594381
VERSION　　AW594381.1　GI:7281639
KEYWORDS　EST.
SOURCE　　Homo sapiens (human)
ORGANISM　Homo sapiens
　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　1　(bases 1 to 397)
AUTHORS　NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE　　National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
　　　　Tumor Gene Index
JOURNAL　Unpublished (1997)
COMMENT　Contact: Robert Strausberg, Ph.D.
　　　　Email: cgapbs-r@mail.nih.gov
　　　　Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
　　　　R. Emmert-Buck, M.D., Ph.D.
　　　　cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
　　　　Bonaldo, Ph.D.
　　　　cDNA Library Arrayed by: Greg Lennon, Ph.D.
　　　　DNA Sequencing by: Washington University Genome Sequencing Center
　　　　Clone distribution: NCI-CGAP clone distribution information can be
　　　　found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 397.

FEATURES
    source
        Location/Qualifiers
        1..397
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2950790"
        /tissue_type="pooled germ cell tumors"
        /lab_host="DH10B"
        /clone_lib="NCI_CGAP_GC4"
        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
        polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
        from the normalized library NCI_CGAP_GC4 was prepared, and
        ss circles were made as tracer in a subtractive hybridization
        reaction. The driver was PCR-amplified cDNAs from a pool
        of 5,000 clones made from the same library (cloneIDs
        1257096-1258631, 1469064-1470983, and 1475592-1476743).
        Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:
Pred. No.:   2.49e-07
Score: 136.00   Length: 397
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 10   Indels: 0
                                       Gaps: 0

US-09-976-740-20 (1-26) x AW594381 (1-397)

Qy   1 GluGluGluGluAspAspAspGluAspGluAspGluAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 177 GAAGAGGAGGAAGATGATGATGAAGAAGATGAAGAAGATGTCAGAGGGCTCT 236

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 237 GAAGTGCCCGAGAGTGAC 254

RESULT 14
LOCUS   AW134620
AW134620
UI-H-B1-abo-f-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
DEFINITION AW134620   412 bp   mRNA   linear   EST 28-OCT-1999
IMAGE:2712710 3', mRNA sequence.
ACCESSION   AW134620
VERSION   AW134620.1 GI:6138166
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 412)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NCI-CGAP clone distribution
            information can be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 82-133,
            >GC_rich#Low complexity 143-219, >(GAA)n#Simple_repeat
            PolyA=No.
            Seq primer: M13 Forward

FEATURES
    source
        Location/Qualifiers
        1..412

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2712710"
/lab_host="DH10B (life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from Bi. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP libraries:
NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid11, NCI_CGAP_Kid12,
NCI_CGAP_Br2, NCI_CGAP_Br23, NCI_CGAP_Co8, NCI_CGAP_Li11, NCI_CGAP_Lei2,
NCI_CGAP_Lu19, NCI_CGAP_Lu24, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1323376-1323911,
1456008-1456775, 1500552-15028855); NCI_CGAP_Kids_pool 1
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lu5 pool 1   LLAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4
pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,
1101192-1101959, 1217928-1217928 1206615); NCI_CGAP_Co10 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255,
1144584-1145351). Subtraction was performed as previously
described [Bonaldo, Lennon & Soares (1996): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Discovery. Genome Research 6, 791-806.
TAG_TISSUE=brain
TAG_LIB=NCI_CGAP_Brn26
TAG_SEQ=ATAGG"

ORIGIN

Alignment Scores:
Pred. No.:   2.59e-07
Score: 136.00   Length: 412
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 10   Indels: 0
                                       Gaps: 0

US-09-976-740-20 (1-26) x AW134620 (1-412)

Qy   1 GluGluGluGluAspAspAspGluAspGluAspGluAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 176 GAAGAGGAGGAAGATGATGATGAAGAAGATGAAGAAGATGTCAGAGGGCTCT 235

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 236 GAAGTGCCCGAGAGTGAC 253

RESULT 15
AI097526
LOCUS   AI097526   429 bp   mRNA   linear   EST 26-OCT-1998
DEFINITION qb87g10.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:1707138 3', similar to contains TAR1.b2 PTR5 repetitive
            element ; , mRNA sequence.
ACCESSION   AI097526
VERSION   AI097526.1 GI:3447108
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 429)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 956   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 421.
FEATURES   Location/Qualifiers
     source   1..429
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1707138"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /note="Organ: heart; Vector: pT7T3D (pharmacia) with a
                     modified polylinker; Site_1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGGACGGCGCCCATCTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library was constructed from the
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
ORIGIN

Alignment Scores:
Pred. No.:   2.72e-07
Score: 136.00   Length: 429
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                                  Gaps: 0

US-09-976-740-20 (1-26) x AI097526 (1-429)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspGluAspAspValSerGluGlySer 20
          | | | | | | | | | | | | | | | | | | | |
Db   159 GAAGAAGGAAGAAGATGAATGAAGAAGATGAAGAAGATGAAGAATGATGTGTCAGAGGGCTCT 218

Qy   21 GluValProGluSerAsp 26
          | | | | | | | | | |
Db   219 GAAGTGCCCGAGAGTGAC 236

Search completed: March 13, 2004, 04:01:36
Job time : 393.119 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:49:56 ; Search time 167.073 Seconds
                                          (without alignments)
                                          2853.675 Million cell updates/sec

Sequence:
Perfect score: 54
Title: US-09-976-740-21
                 1 VSEGSEVPESD 11

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext   0.5
                 Ygapop 10.0 , Ygapext   0.5
                 Fgapop 6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US0976740/runat 10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0997674O @CGN 1.1_9705 @runat 10032004_094548 19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
          1: gb_ba:*
          2: gb_htg:*
          3: gb_in:*
          4: gb_om:*
          5: gb_ov:*
          6: gb_pat:*
          7: gb_ph:*
          8: gb_pl:*
          9: gb_pr:*
         10: gb_ro:*
         11: gb_sts:*
         12: gb_sy:*
         13: gb_un:*
         14: gb_vi:*
         15: gb_ba:*
         16: gb_fun:*
         17: gb_hum:*
         18: gb_in:*
         19: gb_mu:*
         20: gb_Om:*
         21: gb_or:*
         22: gb_pl:*
         23: gb_pat:*
         24: gb_ph:*
         25: gb_pl:*
         26: em_ro:*
         27: em_sts:*
         28: em_un:*
         29: em_vi:*
         30: em_hum:*
         31: em_htg_inv:*
         32: em_htg_other:*
         33: em_htg_mus:*
         34: em_htg_pln:*
         35: em_htg_rod:*
         36: em_htg_mam:*
         37: em_htg_vrt:*
         38: em_sy:*
         39: em_htgo_hum:*
         40: em_htgo_mus:*
         41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	33	6	AR199540	AR199540 Sequence
2	54	100.0	33	6	AR374692	AR374692 Sequence
3	54	100.0	33	6	AR409327	AR409327 Sequence
4	54	100.0	33	6	AX239589	AX239589 Sequence
5	54	100.0	33	6	BD056454	BD056454 Novel low
6	54	100.0	36	6	AR199546	AR199546 Sequence
7	54	100.0	36	6	AR374698	AR374698 Sequence
8	54	100.0	36	6	AR409333	AR409333 Sequence
9	54	100.0	36	6	AX239595	AX239595 Sequence
10	54	100.0	36	6	BD056460	BD056460 Novel low
11	54	100.0	78	6	AR199539	AR199539 Sequence
12	54	100.0	78	6	AR374691	AR374691 Sequence
13	54	100.0	78	6	AR409326	AR409326 Sequence
14	54	100.0	78	6	AX239588	AX239588 Sequence
15	54	100.0	78	6	BD056453	BD056453 Novel low
16	54	100.0	84	6	AR199545	AR199545 Sequence
17	54	100.0	84	6	AR374697	AR374697 Sequence
18	54	100.0	84	6	AR409332	AR409332 Sequence
19	54	100.0	84	6	AX239594	AX239594 Sequence
20	54	100.0	84	6	BD056459	BD056459 Novel low
21	54	100.0	982	9	BC007384	BC007384 Homo sapi
22	54	100.0	1208	6	AR199535	AR199535 Sequence
23	54	100.0	1208	6	AR374687	AR374687 Sequence
24	54	100.0	1208	6	AR409322	AR409322 Sequence
25	54	100.0	1208	6	AX239570	AX239573 Sequence
26	54	100.0	1208	6	BD056449	BD056449 Novel low
27	54	100.0	1362	6	AR199531	AR199531 Sequence
28	54	100.0	1362	6	AR374683	AR374683 Sequence
29	54	100.0	1362	6	AR409318	AR409318 Sequence
30	54	100.0	1362	6	AX239569	AX239569 Sequence
31	54	100.0	1362	6	BD056445	BD056445 Novel low
32	54	100.0	1422	6	AR199532	AR199532 Sequence
33	54	100.0	1422	6	AR374684	AR374684 Sequence
34	54	100.0	1422	6	AR409319	AR409319 Sequence
35	54	100.0	1422	6	AX239570	AX239570 Sequence
36	54	100.0	1422	6	BD056446	BD056446 Novel low
37	54	100.0	1470	9	BC030129	BC030129 Homo sapi
38	54	100.0	1614	6	AR409337	AR409337 Sequence
39	54	100.0	1614	6	AR199530	AR199530 Sequence
40	54	100.0	1617	6	AR199930	AR199930 Sequence
41	54	100.0	1617	6	AR374682	AR374682 Sequence
42	54	100.0	1617	6	AR374682	AR374682 Sequence
43	54	100.0	1617	6	AX239568	AX239568 Sequence
44	54	100.0	1617	6	BD056444	BD056444 Novel low
45	54	100.0	1617	9	AY453840	AY453840 Homo sapi

RESULT 1

```
LOCUS       AR199540                  33 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 32 from patent US 6355451.
ACCESSION   AR199540
VERSION     AR199540.1  GI:20249614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 32 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
```

Alignment Scores:
Pred. No.:
Score: 0.00285
Percent Similarity: 54.00   Length: 33
Best Local Similarity: 100.00%   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                                 Gaps: 0

US-09-976-740-21 (1-11) x AR199540 (1-33)

```
Qy          1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db          1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33
```

RESULT 2

```
LOCUS       AR374692                  33 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 32 from patent US 6605588.
ACCESSION   AR374692
VERSION     AR374692.1  GI:40077507
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 32 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

Alignment Scores:
Pred. No.:
Score: 0.00285
Percent Similarity: 54.00   Length: 33
Best Local Similarity: 100.00%   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                                 Gaps: 0

US-09-976-740-21 (1-11) x AR374692 (1-33)

```
Qy          1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db          1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33
```

RESULT 3

```
LOCUS       AR409327                  33 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence 32 from patent US 6632923.
ACCESSION   AR409327
VERSION     AR409327.1  GI:40160115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 32 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

Alignment Scores:
Pred. No.:
Score: 0.00285
Percent Similarity: 54.00   Length: 33
Best Local Similarity: 100.00%   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                                 Gaps: 0

US-09-976-740-21 (1-11) x AR409327 (1-33)

```
Qy          1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db          1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33
```

RESULT 4

```
LOCUS       AX239589                  33 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 32 from patent WO0164874.
ACCESSION   AX239589
VERSION     AX239589.1  GI:15797265
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 32 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

Alignment Scores:
Pred. No.:
Score: 0.00285
Percent Similarity: 54.00   Length: 33
Best Local Similarity: 100.00%   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                                 Gaps: 0

US-09-976-740-21 (1-11) x AX239589 (1-33)

```
Qy          1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db          1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33
```

RESULT 5

```
LOCUS       BD056454                  33 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Novel low density lipoprotein binding proteins and their use in
```

ACCESSION   BD056454
VERSION   BD056454.1 GI:22602060
KEYWORDS   JP 2001506983-A/12.
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 33)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 12 29-MAY-2001;
            BOSTON HEART FOUNDATION INC
COMMENT
  PN   JP 2001506983-A/12
  PD   29-MAY-2001
  PF   26-NOV-1997 JP 1998524870
  PR   27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
       ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
       A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
       C07H21/00,
  PC   C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
  CC   Strandedness: Single;
  CC   Topology: Linear;
  FH   Key   Location/Qualifiers
FEATURES   Location/Qualifiers
     source   1..33
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.00285   Length: 33
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

US-09-976-740-21 (1-11) x BD056454 (1-33)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

RESULT 6
AR199546
LOCUS   AR199546   36 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 38 from patent US 6355451.
ACCESSION   AR199546
VERSION   AR199546.1 GI:20249620
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 36)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 38 12-MAR-2002;
FEATURES   Location/Qualifiers
     source   1..36
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.00311   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0

DB: 6   Gaps: 0

US-09-976-740-21 (1-11) x AR199546 (1-36)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 7
AR374698
LOCUS   AR374698   36 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6605588.
ACCESSION   AR374698
VERSION   AR374698.1 GI:40077513
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 36)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 38 12-AUG-2003;
FEATURES   Location/Qualifiers
     source   1..36
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.00311   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

US-09-976-740-21 (1-11) x AR374698 (1-36)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 8
AR409333
LOCUS   AR409333   36 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6632923.
ACCESSION   AR409333
VERSION   AR409333.1 GI:40160121
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 36)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 38 14-OCT-2003;
FEATURES   Location/Qualifiers
     source   1..36
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.00311   Length: 36
Percent Similarity: 100.00%   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

RESULT 9

Qy AX239595
Db

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGGCTCGGAGGTGCCCGAGAGCGAT 36

LOCUS   AX239595   36 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION Sequence 38 from Patent WO0164874.
ACCESSION   AX239595
VERSION   AX239595.1 GI:15797271
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 38 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..36
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

US-09-976-740-21 (1-11) x AX239595 (1-36)

Alignment Scores:
Pred. No.:
Score: 0.00311   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 10

Qy BD056460
Db

LOCUS   BD056460   36 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis,.
ACCESSION   BD056460
VERSION   BD056460.1 GI:22602066
KEYWORDS
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 36)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 18 29-MAY-2001;
            BOSTON HEART FOUNDATION INC
COMMENT
            PN   JP 2001506983-A/18
            PD   29-MAY-2001
            PF   26-NOV-1997 JP 199852487O
            PR   27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
            ANN M LEES,ROBERT S LEES,SIMON W LAW ANIBAL A ARJONA PC
            A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
            C07H21/00,
            PC C07X7/00,C07X14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
            Strandedness: Single;
            CC Topology: Linear
            FH Key   Location/Qualifiers
FEATURES   Location/Qualifiers
     source   1..36
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

RESULT 11

Qy AR199539
Db

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGGCTCGGAGGTGCCCGAGAGCGAT 36

LOCUS   AR199539   36 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 31 from patent US 6355451.
ACCESSION   AR199539
VERSION   AR199539.1 GI:20249613
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 31 12-MAR-2002;
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="unknown"
                     /mol_type="unassigned DNA"

US-09-976-740-21 (1-11) x AR199539 (1-78)

Alignment Scores:
Pred. No.:
Score: 0.00311   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db   4 GTGTCCGAGGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 12

Qy AR374691
Db

Db 46 GTGTCAGAGGGGCTCTGAAGTGCCCGAGAGTGAC 78

LOCUS   AR374691   78 bp   DNA   linear   PAT 16-DEC-2003
DEFINITION Sequence 31 from patent US 6605588.
ACCESSION   AR374691
VERSION   AR374691.1 GI:40077506
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 31 12-AUG-2003;
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="unknown"

US-09-976-740-21 (1-11) x AR374691 (1-78)

Alignment Scores:
Pred. No.:
Score: 0.00694   Length: 78
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db 46 GTGTCAGAGGGGCTCTGAAGTGCCCGAGAGTGAC 78

ORIGIN
           /mol_type="genomic DNA"

RESULT 13
LOCUS   AR409326
DEFINITION Sequence 31 from patent US 6632923.   78 bp   DNA   linear   PAT 18-DEC-2003
ACCESSION   AR409326
VERSION   AR409326.1 GI:40160114
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
           diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 31 14-OCT-2003;
FEATURES
     source   1..78
           /organism="unknown"
           /mol_type="genomic DNA"
           Location/Qualifiers

Alignment Scores:
Pred. No.:   0.00694   Length: 78
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 6   Gaps: 0

US-09-976-740-21 (1-11) x AR374691 (1-78)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
    |||:|:||||||||||||||||||
Db 46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

ORIGIN

RESULT 14
LOCUS   AX239588
DEFINITION Sequence 31 from Patent WO0164874. 78 bp   DNA   linear   PAT 26-SEP-2001
ACCESSION   AX239588
VERSION   AX239588.1 GI:15797264
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
           and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 31 07-SEP-2001;
           Boston Heart Foundation, Inc. (US)
FEATURES
     source   1..78
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           Location/Qualifiers

Alignment Scores:
Pred. No.:   0.00694   Length: 78
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 6   Gaps: 0

US-09-976-740-21 (1-11) x AR409326 (1-78)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
    |||:|:||||||||||||||||||
Db 46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

ORIGIN

RESULT 15
LOCUS   BD056453
DEFINITION Novel low density lipoprotein binding proteins and treating 78 bp DNA   linear PAT 27-AUG-2002
           atherosclerosis,.
ACCESSION   BD056453
VERSION   BD056453.1 GI:22602059
KEYWORDS   JP 2001506983-A/11.
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
           Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
           Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
           diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 11 29-MAY-2001;
           BOSTON HEART FOUNDATION INC
COMMENT   PN JP 2001506983-A/11
          PD 29-MAY-2001
          PF 26-NOV-1997 JP 1998524870
          PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
          ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
          A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
          C07H21/00,
          PC C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
          Strandedness: Single; CC
          Topology: Linear; FH
          Key   Location/Qualifiers
FEATURES
     source   1..78
           /organism="Aequorea victoria"
           /mol_type="genomic DNA"
           /db_xref="taxon:6100"

Alignment Scores:
Pred. No.:   0.00694   Length: 78
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 6   Gaps: 0

US-09-976-740-21 (1-11) x AX239588 (1-78)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
    |||:|:||||||||||||||||||
Db 46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

ORIGIN
           /db_xref="taxon:9606"

US-09-976-740-21 (1-11) x BD056453 (1-78)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
    |||:|:||||||||||||||||||
Db 46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

Search completed: March 13, 2004, 00:35:26
Job time : 167.073 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:48:14 ; Search time 17.4357 Seconds
                 (without alignments)
                 2680.137 Million cell updates/sec

Title: US-09-976-740-21
Perfect score: 54
Sequence: 1 VSEGSEVPBSD 11

Scoring table: BLOSUM62
                 Xgapop 10.0 : Xgapext 0.5
                 Ygapop 10.0 : Ygapext 0.5
                 Fgapop 6.0 : Fgapext 0.5
                 Delop   6.0 ; Delext 7.0

Searched: 3373863 seqs, 212409904l residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US0976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -CUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0976740 @CGN_1_1596 @runat_10032004_094547_19532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=7 -YGAPOP=10 -DELOP=6 -DELEXT=7

Database :   N Geneseq_29Jan04:*
             1:   geneseqn1980s:*
             2:   geneseqn1990s:*
             3:   geneseqn2000s:*
             4:   geneseqn2001as:*
             5:   geneseqn2001bs:*
             6:   geneseqn2002s:*
             7:   geneseqn2003as:*
             8:   geneseqn2003bs:*
             9:   geneseqn2003cs:*
            10:   geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	33	5	AAH26504	Aah26504 Low densi
2	54	100.0	36	5	AAH26510	Aah26510 Low densi
3	54	100.0	78	5	AAH26503	Aah26503 Low densi
4	54	100.0	84	5	AAH26509	Aah26509 Low densi
5	54	100.0	1208	5	AAV32838	Aav32838 Human low
6	54	100.0	1208	5	AAH26494	Aah26494 Human low
7	54	100.0	1336	3	AAF21860	Aaf21860 Human bre
8	54	100.0	1362	5	AAH26489	Aah26489 Rabbit lo
9	54	100.0	1422	5	AAH26490	Aah26490 Rabbit lo
10	54	100.0	1614	5	AAH26499	Aah26499 Human low
11	54	100.0	1617	2	AAV32835	Aav32835 Rabbit lo
12	54	100.0	1617	5	AAH26488	Aah26488 Rabbit lo
13	54	100.0	2561	5	AAH26500	Aah26500 Rabbit lo
14	54	100.0	12425	5	AAH26495	Aah26495 Human low
15	41	75.9	378	5	AAF64847	Aaf64847 Novel hum
16	41	75.9	2512	5	ADC27704	Adc27704 Human col
17	41	74.1	374	3	AAC16147	Aac16147 Human sec
18	40	74.1	2428	9	ADB63004	Adb63004 Human cDN
19	40	74.1	3166	7	ABT42108	Abt42108 Toxicity
20	40	74.1	3166	9	ADB58482	Adb58482 Toxicity-
21	40	74.1	3166	9	ADB53074	Adb53074 Primary r
22	39	72.2	1245	4	AAS23121	Aas23121 DNA encod
23	39	72.2	3248	4	AAS23248	Aas23248 Human BMP
24	39	72.2	11446	4	AAK90464	Aak90464 Human dig
25	39	72.2	14759	6	AAD45087	Aad45087 Human bon
26	39	72.2	14759	6	AAD35955	Aad35955 Human bon
27	39	72.2	6728	6	ABQ08179	Abq08179 Human bon
28	38	72.2	160771	6	ABQ88179	Abq88179 Human ost
29	38	70.4	405	8	ADA48469	Ada48469 Rice gene
30	38	70.4	411	6	AAA69711	Aaa69711 Human ova
31	38	70.4	411	8	ADA08770	Ada08770 Human ova
32	38	70.4	411	8	ABN72605	Abn72605 Ovarian c
33	38	70.4	414	6	AAA69763	Aaa69763 Human ova
34	38	70.4	414	8	ABN72657	Abn72657 Ovarian c
35	38	70.4	414	8	ADA08822	Ada08822 Human ova
36	38	70.4	447	7	ABZ52977	Abz52977 Aspergill
37	38	70.4	471	7	AAH30503	Aah30503 Human col
38	38	70.4	495	8	ACH14529	Ach14529 Human adu
39	38	70.4	672	2	AAH31119	Aah31119 Human ova
40	38	70.4	782	3	AAC96936	Aac96936 Human col
41	38	70.4	1178	7	ABZ67115	Abz67115 Human sec
42	38	70.4	1178	7	ABZ73508	Abz73508 Secreted
43	38	70.4	1181	7	ABZ67870	Abz67870 Human sec
44	38	70.4	1181	7	ABZ74310	Abz74310 Secreted
45	38	70.4	1618	9	ADB53270	Adb53270 Primary r

ALIGNMENTS

RESULT 1
AAH26504
ID   AAH26504 standard; DNA; 33 BP.
XX
AC   AAH26504;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS   Mammalia.
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051849.
PR   14-JUL-2000; 2000US-0061289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX
CC   Disclosure; Page 9; 143pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB82797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 33 BP; 7 A; 7 C; 13 G; 6 T; 0 U; 0 Other;

US-09-976-740-21 (1-11) x AAH26504 (1-33)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11

Db   1 GTGTCAGAGGGCTCTGAAGTGCCCAGAGAGTGAC 33

Alignment Scores:

Pred. No.:	1	Length:	33
Score:	0.00767	Matches:	11
Percent Similarity:	54.00	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

RESULT 2
AAH26510
ID   AAH26510 standard; DNA; 36 BP.
XX
AC   AAH26510;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS   Mammalia.
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784 9.
PR   14-JUL-2000; 2000US-0061 6289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Disclosure; Page 10; 143pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB82797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent

---

CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 36 BP; 5 A; 9 C; 16 G; 6 T; 0 U; 0 Other;
XX

US-09-976-740-21 (1-11) x AAH26510 (1-36)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11

Db   4 GTGTCCGAGGGGCTCGGAGGTGCCCGAGAGCGAT 36

Alignment Scores:

Pred. No.:	1	Length:	36
Score:	0.00847	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

RESULT 3
AAH26503
ID   AAH26503 standard; DNA; 78 BP.
XX
AC   AAH26503;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS   Mammalia.
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784 9.
PR   14-JUL-2000; 2000US-0061 6289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Disclosure; Page 9; 143pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB82797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 78 BP; 29 A; 7 C; 29 G; 13 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1	Length:	78
Score:	0.0204	Matches:	11
	54.00	

```
Percent Similarity:         100.00%        Conservative:    0
Best Local Similarity:      100.00%        Mismatches:      0
Query Match:                100.00%        Indels:          0
DB:                         5              Gaps:            0

US-09-976-740-21 (1-11) x AAH26503 (1-78)

Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   46 GTGTCAGGAGGGCTCGAAGTGCCCGAGAGTGAC 78
```

RESULT 4

```
AC   AAH26509;
ID   AAH26509 standard; DNA; 84 BP.
XX
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
OS   Mammalia.
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-0061289.
XX
DR   WPI; 2001-565505/63.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Disclosure; Page 10; 14pp; English.

     The present sequence is that of a polynucleotide encoding a fragment of
     novel low density lipoprotein binding proteins (LBPs) of the invention
     (see AAB82797-820). LBPs are capable of binding to native and methylated
     low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
     LBPs and their fragments are claimed, as well as expression vectors,
     cells and methods of producing the LBPs. Methods of determining if an
     animal is at risk for atherosclerosis, methods for treating an agent
     for use in treating atherosclerosis, and methods for treating a cell
     having an abnormality in structure or metabolism of LBP are also claimed,
     as are pharmaceutical compositions comprising an LBP polypeptide or
     nucleic acid, and vaccine compositions

SQ   Sequence 84 BP; 22 A; 16 C; 40 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                      0.0222         Length:          84
Percent Similarity:         54.00          Matches:         11
Best Local Similarity:      100.00%        Conservative:    0
Percent Similarity:         100.00%        Mismatches:      0
Query Match:                100.00%        Indels:          0
DB:                         5              Gaps:            0

US-09-976-740-21 (1-11) x AAH26509 (1-84)

Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   52 GTGTCCGAGGGGCTCGGAGGGTGCCCGAGAGCGAT 84
```

RESULT 5

```
AC   AAV32838
ID   AAV32838 standard; cDNA; 1208 BP.
XX
XX
AC   AAV32838;
XX
DT   09-NOV-1998 (first entry)
XX
DE   Human low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW   receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   CDS             1..654
FT                   /tag= a
FT   misc_feature    22..99
FT                   /tag= c
FT                   /note= "Claim 13"
FT   misc_feature    22..66
FT                   /tag= b
FT                   /note= "Claim 12"
FT   misc_feature    67..99
FT                   /tag= d
FT                   /note= "Claim 14"
FT   misc_feature    622..651
FT                   /tag= e
FT                   /note= "Claim 15"
XX
PN   WO9823282-A1.
XX
PD   04-JUN-1998.
XX
PF   26-NOV-1997; 97WO-US021857.
XX
PR   27-NOV-1996; 96US-0031930P.
PR   03-JUN-1997; 97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49041.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 9; Fig 16; 47pp; English.

     This cDNA clone codes for novel human low density lipoprotein (LDL)
     binding protein LBP-2 (see AAW49041). It was isolated by screening human
     liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA
     clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
     42) are claimed. An abnormality in LBP metabolism or structure is
     diagnostic of a risk for atherosclerosis. The invention provides: methods
     for determining if an animal is at risk for atherosclerosis (including
     prenatal screening); methods for treating atherosclerosis (e.g. for
     therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
     formation of atherosclerotic plaque; and methods for treating a cell
     having an abnormality in LBP structure or metabolism. Pharmaceutical and
     vaccine compositions are also provided, as well as recombinant vectors
     and host cells used to produce recombinant LBP

SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:
Score:                      0.463          Length:          1208
```

RESULT 6
AAH26494
ID   AAH26494 standard; cDNA; 1208 BP.
XX
AC   AAH26494;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiateriosclerotic; gene therapy; diagnosis; vaccine;
ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..654
FT   /*tag= a
FT   /partial
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784 9.
PR   14-JUL-2000; 2000US-0061628 9.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82803.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 4; Fig 16; 143pp; English.
XX
CC   The present sequence is that of a partial cDNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC   isolated from human foetal brain, liver and aorta cDNA libraries using
CC   rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC   AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides capable of binding to native and methylated LDL. Also
CC   claimed are isolated LBP polypeptides, and biologically active fragments
CC   or analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, methods for evaluating an agent for use in treating
CC   atherosclerosis, and methods for treating a cell having an abnormality in
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed.
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db   67 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 99

US-09-976-740-21 (1-11) x AAV32838 (1-1208)

Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 2   Gaps: 0

RESULT 7
AAF21860
ID   AAF21860 standard; DNA; 1336 BP.
XX
AC   AAF21860;
XX
DT   27-MAR-2001 (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 247.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005881.
XX
PR   12-MAR-1999; 99US-01242707.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58957.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention, treatment
PT   and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT   neurological diseases.
XX
PS   Claim 1; Page 670-671; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemias; wound healing;

Pred. No.:   0.463   Length: 1208
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 5   Gaps: 0

US-09-976-740-21 (1-11) x AAH26494 (1-1208)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||
Db   67 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 99

CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
XX
SQ Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;
XX

Alignment Scores:

Pred. No.:			
Score:	0.519	Length:	1336
Percent Similarity:	54.00	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	3	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x AAF21860 (1-1336)

Qy 1 ValSerGlyGlySerGluValProGluSerAsp 11
   |||||||||||||||||||||||||||||||||||
Db 139 GTGTCCAGAGGGGCTCTCAAGTGCCCGAGAGTCAC 171

RESULT 8
ID AAH26489
  AAH26489 standard; cDNA; 1362 BP.
XX
AC AAH26489;
XX
DT 12-NOV-2001 (first entry)
XX
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..955
FT   /*tag= a
FT   /partial
XX
PN WO200164874-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-00517849.
PR 14-JUL-2000; 2000US-0061629.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT New isolated low density lipoprotein binding polypeptide for treating,
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
DR WPI; 2001-565505/63.
DR P-PSDB; AAB82799.
XX
PS Example 2; Fig 12; 143pp; English.
XX

The present sequence is that of cDNA encoding a portion (see AAB82799) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an

---

CC abnormality in structure or metabolism of LBP. Pharmaceutical
CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC compositions, are also claimed
XX
SQ Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;
XX

Alignment Scores:

Pred. No.:			
Score:	0.531	Length:	1362
Percent Similarity:	54.00	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	5	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x AAH26489 (1-1362)

Qy 1 ValSerGlyGlySerGluValProGluSerAsp 11
   |||||||||||||||||||||||||||||||||||
Db 109 GTGTCCGAGGGGCTCGGAGGGTGCCCGAGAGGGAT 141

RESULT 9
ID AAH26490
  AAH26490 standard; cDNA; 1422 BP.
XX
AC AAH26490;
XX
DT 12-NOV-2001 (first entry)
XX
DE Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.
XX
KW Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..955
FT   /*tag= a
FT   /partial
XX
PN WO200164874-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-00517849.
PR 14-JUL-2000; 2000US-0061629.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT New isolated low density lipoprotein binding polypeptide for treating,
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
DR WPI; 2001-565505/63.
DR P-PSDB; AAB82800.
XX
PS Example 2; Fig 13; 143pp; English.
XX

The present sequence is that of cDNA encoding a portion (see AAB82800) of novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in AAH26491. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent

```
CC     for use in treating atherosclerosis, and methods for treating a cell
CC     having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC     compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC     compositions, are also claimed
XX
SQ     Sequence 1422 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                   0.557          Length:         1422
Score:                      54.00           Matches:          11
Percent Similarity:        100.00%          Conservative:      0
Best Local Similarity:     100.00%          Mismatches:        0
Query Match:                    5           Indels:            0
DB:                                         Gaps:              0

US-09-976-740-21 (1-11) x AAH26490 (1-1422)

Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db  169 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 201

RESULT 10
AAH26499
ID     AAH26499 standard; DNA; 1614 BP.
XX
AC     AAH26499;
XX
DT     12-NOV-2001 (first entry)
XX
DE     Human low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW     Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW     atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW     ds.
XX
OS     Homo sapiens.
XX
PN     WO20016874-A2.
XX
PD     07-SEP-2001.
XX
PF     28-FEB-2001; 2001WO-US006356.
XX
PR     02-MAR-2000; 2000US-0051789.
PR     14-JUL-2000; 2000US-0016289.
XX
PA     (BOST-) BOSTON HEART FOUND INC.
XX
PI     Lees AM,  Lees RS,  Law SW,  Arjona AA;
XX
DR     WPI; 2001-565505/63.
DR     P-PSDB; AAB82806.
XX
PT     Claim 7; Fig 7A; 143pp; English.
```

The present sequence is that of the coding region of the human gene (see also AAH26494) encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the present sequence differs from that predicted from a cDNA clone (see AAB82803) in that it contains an additional 321 amino acids at its N-terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions

```
CC     comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC     are also claimed
XX
SQ     Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                   0.644          Length:         1614
Score:                      54.00           Matches:          11
Percent Similarity:        100.00%          Conservative:      0
Best Local Similarity:     100.00%          Mismatches:        0
Query Match:                    5           Indels:            0
DB:                                         Gaps:              0

US-09-976-740-21 (1-11) x AAH26499 (1-1614)

Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db 1030 GTGTCAGAGGGGCTCTGAAGTGCCCGAGAGTGAC 1062

RESULT 11
AAV32835
ID     AAV32835 standard; cDNA; 1617 BP.
XX
AC     AAV32835;
XX
DT     09-NOV-1998 (first entry)
XX
DE     Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX
KW     Low density lipoprotein binding protein; LDL, binding protein 2; LBP-2;
KW     receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS     Oryctolagus cuniculus.
XX
FH     Key            Location/Qualifiers
FT     CDS            1..954
FT                    /*tag= a
FT     misc_feature   156..1617
FT                    /*tag= b
FT     misc_feature   156..954
FT                    /*tag= d
FT                    /note= "Claim 5"
FT     misc_feature   196..1617
FT                    /*tag= c
FT                    /note= "Claim 6"
FT     misc_feature   313..396
FT                    /*tag= e
FT                    /note= "Claim 5"
FT     misc_feature   313..360
FT                    /*tag= f
FT                    /note= "Claim 19"
FT     misc_feature   313..360
FT                    /*tag= e
FT                    /note= "Claim 18"
FT     misc_feature   361..396
FT                    /*tag= g
FT                    /note= "Claim 20"
FT     misc_feature   631..660
FT                    /*tag= h
FT                    /note= "Claim 21"
XX
PN     WO9823282-A1.
XX
PD     04-JUN-1998.
XX
PF     26-NOV-1997; 97WO-US021857.
XX
PR     27-NOV-1996; 96US-0031930P.
PR     03-JUN-1997; 97US-0048547P.
XX
PA     (BOST-) BOSTON HEART FOUND INC.
XX
PI     Lees AM,  Lees RS,  Law SW,  Arjona AA;
XX
DR     WPI; 1998-322455/28.
```

DR   P-PSDB; AAW49038.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 4; Fig 11; 47pp; English.
XX
CC   This cDNA clone codes for novel rabbit low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49038). It was isolated by functional
CC   screening of a cDNA library, produced from balloon-deendothelialised
CC   healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to
CC   bind both native and methyl LDL. cDNA clones (see AAV32834-39) and
CC   encoded rabbit and human LBPs (see AAW49037-42) are claimed. An
CC   abnormality in an aspect of LBP metabolism or structure is diagnostic of
CC   a risk for atherosclerosis. The invention provides: methods for
CC   determining if an animal is at risk for atherosclerosis (e.g. for
CC   prenatal screening); methods for treating atherosclerosis (including gene
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP
XX
SQ   Sequence 1617 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   0.645
Score: 54.00
Percent Similarity: 100.00%   Matches: 11   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0   Indels: 0
Query Match: 2   Gaps: 0
DB: Length: 1617

US-09-976-740-21 (1-11) x AAV32835 (1-1617)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
Db 364 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 396

RESULT 12
AAH26488
ID   AAH26488 standard; cDNA; 1617 BP.
XX
AC   AAH26488;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag= a
FT   /partial
FT   /note= "includes in-frame stop codon at nucleotides
FT   28..30"
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0517849.
PR   14-JUL-2000; 2000US-0616289.
XX

PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PN   WPI; 2001-565505/63.
DR   P-PSDB; AAB82798.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 11; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82798) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at risk for atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1617 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   0.645
Score: 54.00
Percent Similarity: 100.00%   Matches: 11   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0   Indels: 0
Query Match: 5   Gaps: 0
DB: Length: 1617

US-09-976-740-21 (1-11) x AAH26488 (1-1617)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
Db 364 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 396

RESULT 13
AAH26500
ID   AAH26500 standard; cDNA; 2561 BP.
XX
AC   AAH26500;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   246..1928
FT   /*tag= a
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0517849.
PR   14-JUL-2000; 2000US-0616289.
XX

PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR WPI; 2001-565505/63.
DR P-PSDB; AAB82807.
XX
PN
XX
PT New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS Claim 4; Fig 2A; 143pp; English.
XX
CC The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for treating a cell for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
XX
SQ Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;

US-09-976-740-21 (1-11) x AAH26500 (1-2561)

Alignment Scores:
Pred. No.:   1.09
Score: 54.00
Percent Similarity: 100.00%   Length: 2561
Best Local Similarity: 100.00%   Matches: 11
Query Match: 5   Conservative: 0
                                           Mismatches: 0
                                           Indels: 0
DB: Gaps: 0

Qy 1   ValSerGluGlySerGluValProGluSerAsp 11
Db 1308 GTGTCCGAGGGCTCGAGGTGCCCGAGAGTGGAT 1340

RESULT 14
AAH26495

ID AAH26495 standard; DNA; 12425 BP.
AC AAH26495;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human low density lipoprotein binding protein 2 (LBP-2) gene.
XX
KW Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiatherosclerotic; gene therapy; diagnosis; vaccine;
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FH CDS
FT CDS   2832..5153
FT   /*tag= a
FT exon   2832..3785
FT   /note= "includes introns"
FT   /*tag= b
FT exon   3786..4207
FT   /*tag= c
FT intron   4208..4502
FT   /*tag= d
FT exon   4503..4593
FT   /*tag= e
FT intron   4594..4694
FT   /*tag= f

FT intron   4695..4787
FT   /*tag= g
FT exon   4788..4899
FT   /*tag= h
FT intron   4900..4994
FT   /*tag= i
FT exon   4995..5153
FT   /*tag= j
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
PN WO200164874-A2.
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-00517849.
PR 14-JUL-2000; 2000US-00616289.
XX
DR WPI; 2001-565505/63.
DR P-PSDB; AAB82806.
XX
PT New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS Example 4; Fig 23; 143pp; English.
XX
CC The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
XX
SQ Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

US-09-976-740-21 (1-11) x AAH26495 (1-12425)

Alignment Scores:
Pred. No.:   6.58
Score: 54.00
Percent Similarity: 100.00%   Length: 12425
Best Local Similarity: 100.00%   Matches: 11
Query Match: 5   Conservative: 0
                                           Mismatches: 0
                                           Indels: 0
DB: Gaps: 0

Qy 1   ValSerGluGlySerGluValProGluSerAsp 11
Db 4283 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 4315

RESULT 15
AAF64847;

ID AAF64847 standard; cDNA; 378 BP.
AC AAF64847;
XX
DT 09-APR-2001 (first entry)
XX
DE Novel human polynucleotide, SEQ ID NO: 603.
XX
KW Human; cytostatic; gene therapy; colon cancer; prostate cancer; breast cancer; lung cancer; cancer detection; ss.

```
XX
OS   Homo sapiens.
XX
PN   WO200102568-A2.
XX
PD   11-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018374.
XX
PR   02-JUL-1999;  99US-0142310P.
PR   02-JUL-1999;  99US-0142311P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI   Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI   Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI   Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR   WPI; 2001-091805/10.
XX
PT   Library of polynucleotides for diagnosing a cancerous state of a
PT   mammalian cell and detecting cancer, particularly of the colon or
PT   prostate, comprises 3351 human polynucleotide sequences.
XX
PS   Claim 9; Page 631; 1046pp; English.
XX
CC   The present sequence is one of 3351 sequences in a library of human
CC   polynucleotides. The library is used to detect differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell and can
CC   detect colon, prostate, breast and lung cancer. The library can be used
CC   to produce probes for detection of mRNA and to produce additional copies
CC   of the polynucleotides. The probes can be used for chromosome mapping of
CC   the polynucleotide and for detection of transcription levels. Ribozymes
CC   or antisense oligonucleotides can be generated. The polynucleotides and
CC   their gene products are used as genetic or biochemical markers (e.g. in
CC   blood or tissues) that will detect the earliest changes along the
CC   carcinogenesis pathway and/or monitor the efficacy of therapies and
CC   preventive interventions. The polynucleotides, polypeptides and
CC   antibodies against them can be used in pharmaceutical compositions to
CC   treat the cancers and proliferative disorders such as neoplasia,
CC   dysplasia and hyperplasia
XX
SQ   Sequence 378 BP; 95 A; 95 C; 83 G; 105 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:            47.3
Score:               41.00           Length:         378
Percent Similarity:  90.91%          Matches:          8
Best Local Similarity: 72.73%        Conservative:     2
Query Match:         75.93%          Mismatches:       1
DB:                  5               Indels:           0
                                     Gaps:             0
```

```
US-09-976-740-21 (1-11) x AAF64847 (1-378)

Qy     1 ValSerGluGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||:::::
Db    55 GTCTCGGAGAATTCAGAGGTGCCAGAAGCCAG 23
```

Search completed: March 12, 2004, 21:08:41
Job time : 23.4357 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 20:05:17 ; Search time 3.7295 Seconds
(without alignments)
1636.805 Million cell updates/sec

Title: US-09-976-740-21
Perfect score: 54
Sequence: 1 VSEGSEVPESD 11

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19564/app_query.fasta_1.1898
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740@CGN_1_1_235 @runat_10032004_094549_19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	33	4	US-08-979-608A-32	Sequence 32, Appl
2	54	100.0	33	4	US-09-517-849-32	Sequence 32, Appl
3	54	100.0	33	4	US-09-616-289-32	Sequence 32, Appl
4	54	100.0	36	4	US-08-979-608A-38	Sequence 38, Appl
5	54	100.0	36	4	US-09-517-849-38	Sequence 38, Appl
6	54	100.0	36	4	US-09-616-289-38	Sequence 38, Appl
7	54	100.0	78	4	US-08-979-608A-31	Sequence 31, Appl
8	54	100.0	78	4	US-09-517-849-31	Sequence 31, Appl
9	54	100.0	78	4	US-09-616-289-31	Sequence 31, Appl
10	54	100.0	84	4	US-08-979-608A-37	Sequence 37, Appl
11	54	100.0	84	4	US-09-517-849-37	Sequence 37, Appl
12	54	100.0	84	4	US-09-616-289-37	Sequence 37, Appl
13	54	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appl
14	54	100.0	1208	4	US-09-517-849-16	Sequence 16, Appl
15	54	100.0	1208	4	US-09-616-289-16	Sequence 16, Appl
16	54	100.0	1362	4	US-08-979-608A-12	Sequence 12, Appl
17	54	100.0	1362	4	US-09-517-849-12	Sequence 12, Appl
18	54	100.0	1362	4	US-09-616-289-12	Sequence 12, Appl
19	54	100.0	1422	4	US-08-979-608A-13	Sequence 13, Appl
20	54	100.0	1422	4	US-09-517-849-13	Sequence 13, Appl
21	54	100.0	1422	4	US-09-616-289-13	Sequence 13, Appl
22	54	100.0	1614	4	US-08-979-608A-45	Sequence 45, Appl
23	54	100.0	1617	4	US-09-517-849-11	Sequence 11, Appl
24	54	100.0	1617	4	US-09-616-289-11	Sequence 11, Appl
25	54	100.0	2561	4	US-09-616-289-48	Sequence 48, Appl
26	54	100.0	12425	4	US-09-616-289-50	Sequence 50, Appl
27	54	100.0	6728	4	US-09-674-459B-1	Sequence 1, Appli
28	39	72.2	14759	4	US-09-661-887-1	Sequence 1, Appli
29	39	72.2	411	4	US-09-404-879A-21	Sequence 21, Appl
30	38	70.4	411	4	US-09-338-933-21	Sequence 21, Appl
31	38	70.4	411	4	US-09-215-681-21	Sequence 21, Appl
32	38	70.4	411	4	US-09-216-003A-21	Sequence 21, Appl
33	38	70.4	414	4	US-09-404-879A-73	Sequence 73, Appl
34	38	70.4	414	4	US-09-338-933-73	Sequence 73, Appl
35	38	70.4	414	4	US-09-215-681-73	Sequence 73, Appl
36	38	70.4	414	4	US-09-216-003A-73	Sequence 73, Appl
37	38	70.4	3090	5	PCT-US93-06251-7	Sequence 7, Appli
38	38	70.4	276	5	US-09-107-532A-65	Sequence 65, Appli
39	36	66.7	1092	4	US-09-107-532A-1437	Sequence 1437, Ap
40	36	66.7	276	4	US-09-266-464-1	Sequence 1, Appli
41	36	66.7	1092	4	US-09-016-434-1095	Sequence 1095, Ap
42	36	66.7	2577	3	US-09-633-768A-3	Sequence 3, Appli
43	36	66.7	2577	3	US-08-633-768A-3	Sequence 3, Appli
44	36	66.7	3267	4	US-09-280-197-3	Sequence 3, Appli
45	35.5	65.7	2268	4	US-09-134-000C-3286	Sequence 3286, Ap

ALIGNMENTS

RESULT 1
US-08-979-608A-32
Sequence 32, Application US/08979608A
Patent No. 6355451
Sequence 32, Application US/08979608A

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
           Lees, Robert S.
           Law, Simon W.
           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
           BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
           TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/979,608A
    FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/048,547
    FILING DATE: 03-JUN-1997
    APPLICATION NUMBER: US 60/031,930
    FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965

```
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 32:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 33 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   FEATURE:
;     NAME/KEY: Coding Sequence
;     LOCATION: 1..33
;   SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-08-979-608A-32

Alignment Scores:
Pred. No.:
Score:                 0.0013
Percent Similarity:    54.00         Length:        33
Best Local Similarity: 100.00%       Matches:       11
Query Match:           100.00%       Conservative:  0
                       4             Mismatches:    0
                                     Indels:        0
                                     Gaps:          0

Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
      ||||||||||||||||||||||||||||||||
Db  1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

US-09-976-740-21 (1-11) x US-08-979-608A-32 (1-33)

RESULT 2
US-09-517-849-32
; Sequence 32, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;             Lees, Robert S.
;             Law, Simon W.
;             Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;                       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;                       TREATING ATHEROSCLEROSIS
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/517,849
;     FILING DATE: 02-Mar-2000
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/979,608
;     FILING DATE: 26-NOV-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Myers, Louis
;     REGISTRATION NUMBER: 35,965
;     REFERENCE/DOCKET NUMBER: 10797-003001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617/542-5070
;     TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 32:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 33 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   FEATURE:
;     NAME/KEY: Coding Sequence
;     LOCATION: 1..33
;   SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-517-849-32

Alignment Scores:
Pred. No.:
Score:                 0.0013
Percent Similarity:    54.00         Length:        33
Best Local Similarity: 100.00%       Matches:       11
Query Match:           100.00%       Conservative:  0
                       4             Mismatches:    0
                                     Indels:        0
                                     Gaps:          0

Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
      ||||||||||||||||||||||||||||||||
Db  1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

US-09-976-740-21 (1-11) x US-09-517-849-32 (1-33)

RESULT 3
US-09-616-289-32
; Sequence 32, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   APPLICANT: Lees, Robert S.
;   APPLICANT: Law, Simon W.
;   APPLICANT: Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;   TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;   TITLE OF INVENTION: ATHEROSCLEROSIS
;   FILE REFERENCE: 10797-004001
;   CURRENT APPLICATION NUMBER: US/09/616,289
;   CURRENT FILING DATE: 2000-07-14
;   PRIOR APPLICATION NUMBER: US 09/517,849
;   PRIOR FILING DATE: 2000-03-02
;   PRIOR APPLICATION NUMBER: US 08/979,608
;   PRIOR FILING DATE: 1997-11-26
;   PRIOR APPLICATION NUMBER: US 60/031,930
;   PRIOR FILING DATE: 1996-11-27
;   PRIOR APPLICATION NUMBER: US 60/048,547
;   PRIOR FILING DATE: 1997-06-03
;   NUMBER OF SEQ ID NOS: 53
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 32
;     LENGTH: 33
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-09-616-289-32

Alignment Scores:
Pred. No.:
Score:                 0.0013
Percent Similarity:    54.00         Length:        33
Best Local Similarity: 100.00%       Matches:       11
Query Match:           100.00%       Conservative:  0
                       4             Mismatches:    0
                                     Indels:        0
                                     Gaps:          0

Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
      ||||||||||||||||||||||||||||||||
Db  1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

US-09-976-740-21 (1-11) x US-09-616-289-32 (1-33)

RESULT 4
US-08-979-608A-38
; Sequence 38, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;              Lees, Robert S.
```

Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No.
PRIOR APPLICATION DATA:
FILING DATE: 26-No.
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..36
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-08-979-608A-38

Alignment Scores:
Pred. No.:
Score: 0.00144   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                     Gaps: 0

US-09-976-740-21 (1-11) x US-08-979-608A-38 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db 4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 5
US-09-517-849-38
Sequence 38, Application US/0951849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEPHONE: 617/542-5070
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..36
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-517-849-38

Alignment Scores:
Pred. No.:
Score: 0.00144   Length: 36
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                     Gaps: 0

US-09-976-740-21 (1-11) x US-09-517-849-38 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||||
Db 4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 6
US-09-616-289-38
Sequence 38, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03

```
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 38
;    LENGTH: 36
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-616-289-38

Alignment Scores:
Pred. No.:                              Length:        36
Score:                  0.00144         Matches:       36
Percent Similarity:     54.00           Conservative:  11
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            100.00%         Indels:        0
DB:                                     Gaps:          0

US-09-976-740-21 (1-11) x US-09-616-289-38 (1-36)

Qy       1 ValSerGluGlySerGluValProGluSerAsp 11
            |||||||||||||||||||||||||||||||||
Db       4 GTGTCCGAGGGCTCCGAGGTGCCCGAGAGCGAT 36

RESULT 7
US-08-979-608A-31
;  Sequence 31, Application US/08979608A
;  Patent No. 6355451
;  GENERAL INFORMATION:
;    APPLICANT: Lees, Ann M.
;              Lees, Robert S.
;              Law, Simon W.
;              Arjona, Anibal A.
;    TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;                       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;                       TREATING ATHEROSCLEROSIS
;    NUMBER OF SEQUENCES: 42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Fish & Richardson P.C.
;      STREET: 225 Franklin Street
;      CITY: Boston
;      STATE: MA
;      COUNTRY: USA
;      ZIP: 02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/979,608A
;      FILING DATE: 26-No. 6355451-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 60/048,547
;      FILING DATE: 03-JUN-1997
;      APPLICATION NUMBER: US 60/031,930
;      FILING DATE: 27-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Myers, Louis
;      REGISTRATION NUMBER: 35,965
;      REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 617/542-5070
;      TELEFAX: 617/542-8906
;    INFORMATION FOR SEQ ID NO: 31:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 78 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      FEATURE:
;        NAME/KEY: Coding Sequence
;        LOCATION: 1..78
;    SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-08-979-608A-31
```

```
Alignment Scores:
Pred. No.:                              Length:        78
Score:                  0.00346         Matches:       11
Percent Similarity:     54.00           Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            100.00%         Indels:        0
DB:                                     Gaps:          0

US-09-976-740-21 (1-11) x US-08-979-608A-31 (1-78)

Qy       1 ValSerGluGlySerGluValProGluSerAsp 11
            |||||||||||||||||||||||||||||||||
Db      46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

RESULT 8
US-09-517-849-31
;  Sequence 31, Application US/09517849
;  Patent No. 6605588
;  GENERAL INFORMATION:
;    APPLICANT: Lees, Ann M.
;              Lees, Robert S.
;              Law, Simon W.
;              Arjona, Anibal A.
;    TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;                       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;                       TREATING ATHEROSCLEROSIS
;    NUMBER OF SEQUENCES: 42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Fish & Richardson P.C.
;      STREET: 225 Franklin Street
;      CITY: Boston
;      STATE: MA
;      COUNTRY: USA
;      ZIP: 02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/517,849
;      FILING DATE: 02-Mar-2000
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/979,608
;      FILING DATE: 26-NOV-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Myers, Louis
;      REGISTRATION NUMBER: 35,965
;      REFERENCE/DOCKET NUMBER: 10797-003001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 617/542-5070
;      TELEFAX: 617/542-8906
;    INFORMATION FOR SEQ ID NO: 31:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 78 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      FEATURE:
;        NAME/KEY: Coding Sequence
;        LOCATION: 1..78
;    SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-517-849-31
```

US-09-976-740-21 (1-11) x US-09-517-849-31 (1-78)

```
Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||
Db   46 GTGTCAGAGGACGGCTCGAAGTGCCCGAGAGTGAC 78
```

RESULT 9
US-09-616-289-31
Sequence 31, Application US/0961629
Patent No. 6632923
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
  TITLE OF INVENTION: ATHEROSCLEROSIS
  FILE REFERENCE: 10797-004001
  CURRENT APPLICATION NUMBER: US/09/616,289
  CURRENT FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: US 09/517,849
  PRIOR FILING DATE: 2000-03-02
  PRIOR APPLICATION NUMBER: US 08/979,608
  PRIOR FILING DATE: 1997-11-26
  PRIOR APPLICATION NUMBER: US 60/031,930
  PRIOR FILING DATE: 1996-11-27
  PRIOR APPLICATION NUMBER: US 60/048,547
  PRIOR FILING DATE: 1997-06-03
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
  LENGTH: 78
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-616-289-31

Alignment Scores:
```
Pred. No.:
Score:                 0.0346          Length:       78
Percent Similarity:    54.00           Matches:      11
Best Local Similarity: 100.00%         Conservative: 0
Query Match:           100.00%         Mismatches:   0
DB:                    4               Indels:       0
                                       Gaps:         0
```

US-09-976-740-21 (1-11) x US-09-616-289-31 (1-78)

```
Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||
Db   46 GTGTCAGAGGGCCTCGAAGTGCCCGAGAGTGAC 78
```

RESULT 10
US-08-979-608A-37
Sequence 37, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
  TITLE OF INVENTION: BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
  TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/979,608A
  FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/048,547
  FILING DATE: 03-JUN-1997
  APPLICATION NUMBER: US 60/031,930
  FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Myers, Louis
  REGISTRATION NUMBER: 35,965
  REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-2906
INFORMATION FOR SEQ ID NO: 37:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 84 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..84
  SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-979-608A-37

Alignment Scores:
```
Pred. No.:
Score:                 0.00377         Length:       84
Percent Similarity:    54.00           Matches:      11
Best Local Similarity: 100.00%         Conservative: 0
Query Match:           100.00%         Mismatches:   0
DB:                    4               Indels:       0
                                       Gaps:         0
```

US-09-976-740-21 (1-11) x US-08-979-608A-37 (1-84)

```
Qy    1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||
Db   52 GTGTCCGAGGGCTCCGAGGTGCCCGAGAGGGAT 84
```

RESULT 11
US-09-517-849-37
Sequence 37, Application US/0951784
Patent No. 6605588
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
  TITLE OF INVENTION: BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
  TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/517,849
  FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..84
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-517-849-37

Alignment Scores:

Pred. No.:		Length:	84
Score:	0.00377	Matches:	11
Percent Similarity:	54.00	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
US-09-517-849-37	4	Gaps:	0

US-09-976-740-21 (1-11) x US-09-517-849-37 (1-84)

```
Qy    1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   52 GTGTCCGAGGGCTCCGAGGGTGCCCGAGAGCGAT 84
```

RESULT 12
US-09-616-289-37
; Sequence 37, Application US/0961628
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;   PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;   ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-37

Alignment Scores:

Pred. No.:		Length:	84
Score:	0.00377	Matches:	11
Percent Similarity:	54.00	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
US-09-616-289-37	4	Gaps:	0

US-09-976-740-21 (1-11) x US-09-616-289-37 (1-84)

```
Qy    1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   52 GTGTCCGAGGGCTCGGAGGGTGCCCGAGAGCGAT 84
```

RESULT 13
US-08-979-608A-16
; Sequence 16, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-No-
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..651
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16

Alignment Scores:

Pred. No.:		Length:	1208
Score:	0.0775	Matches:	11
Percent Similarity:	54.00	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
US-08-979-608A-16	4	Gaps:	0

US-09-976-740-21 (1-11) x US-08-979-608A-16 (1-1208)

```
Qy    1 ValSerGlyGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   67 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 99
```

RESULT 14
US-09-517-849-16
Sequence 16, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
          Lees, Robert S.
          Law, Simon W.
          Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
      BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
      TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/517,849
    FILING DATE: 02-Mar-2000
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/979,608
    FILING DATE: 26-NOV-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965
    REFERENCE/DOCKET NUMBER: 10797-003001
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906
  INFORMATION FOR SEQ ID NO: 16:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1208 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    FEATURE:
      NAME/KEY: Coding Sequence
      LOCATION: 1...651
    SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-517-849-16

US-09-976-740-21 (1-11) x US-09-517-849-16 (1-1208)

Alignment Scores:
Pred. No.:
Score: 0.0775
Percent Similarity: 54.00   Length: 1208
Best Local Similarity: 100.00%   Matches: 11
Query Match: 100.00%   Conservative: 0
DB: 100.00%   Mismatches: 0
           4   Indels: 0
               Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
     |||||||||||||||||||||||||||||||||
Db   67 GTGTCAGAGGGCTCTGAAGTGCCGAGAGTGAC 99

RESULT 15
US-09-616-289-16
Sequence 16, Application US/0961629
Patent No. 663923
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.

  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
  TITLE OF INVENTION: ATHEROSCLEROSIS
  FILE REFERENCE: 10797-004001
  CURRENT APPLICATION NUMBER: US/09/616,289
  CURRENT FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: US 09/517,849
  PRIOR FILING DATE: 2000-03-02
  PRIOR APPLICATION NUMBER: US 08/979,608
  PRIOR FILING DATE: 1997-11-26
  PRIOR APPLICATION NUMBER: US 60/031,930
  PRIOR FILING DATE: 1996-11-27
  PRIOR APPLICATION NUMBER: US 60/048,547
  PRIOR FILING DATE: 1997-06-03
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 16
    LENGTH: 1208
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)...(651)
US-09-616-289-16

US-09-976-740-21 (1-11) x US-09-616-289-16 (1-1208)

Alignment Scores:
Pred. No.:
Score: 0.0775
Percent Similarity: 54.00   Length: 1208
Best Local Similarity: 100.00%   Matches: 11
Query Match: 100.00%   Conservative: 0
DB: 100.00%   Mismatches: 0
           4   Indels: 0
               Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
     |||||||||||||||||||||||||||||||||
Db   67 GTGTCAGAGGGCTCTGAAGTGCCGAGAGTGAC 99

Search completed: March 13, 2004, 04:06:26
Job time : 5.7295 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 20:46:42 ; Search time 15.9143 Seconds
                 (without alignments)
                 2544.725 Million cell updates/sec

Title: US-09-976-740-21
Perfect score: 54
Sequence: 1 VSBGSEVPESD 11

Scoring table: BLOSUM62
                 Xgapop 10.0 ; Xgapext 0.5
                 Ygapop 10.0 ; Ygapext 0.5
                 Fgapop 6.0 ; Fgapext 7.0
                 Delop   6.0 ; Delext 7.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model - DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19588/app_query.fasta_1.1898
-DB=Published Applications NA - QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09976740 @CGN_1_712 @runat_10032004_094549_19588
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG - DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published Applications NA:*
      1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
      2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
      3: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
      4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
      5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
      6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
      7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
      8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
      9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
     10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
     11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
     12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
     13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
     14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
     15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
     16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
     17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
     18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	54	100.0	33	9	US-09-962-055-32	Sequence 32, App1
2	54	100.0	33	9	US-09-976-740-32	Sequence 32, App1
3	54	100.0	33	12	US-10-671-242-32	Sequence 32, App1
4	54	100.0	33	13	US-10-023-529-32	Sequence 32, App1
5	54	100.0	33	13	US-10-023-523-32	Sequence 32, App1
6	54	100.0	33	15	US-10-616-187-32	Sequence 32, App1
7	54	100.0	36	9	US-09-962-055-38	Sequence 38, App1
8	54	100.0	36	9	US-09-976-740-38	Sequence 38, App1
9	54	100.0	36	12	US-10-671-242-38	Sequence 38, App1
10	54	100.0	36	13	US-10-023-529-38	Sequence 38, App1
11	54	100.0	36	13	US-10-023-523-38	Sequence 38, App1
12	54	100.0	36	15	US-09-976-740-31	Sequence 31, App1
13	54	100.0	78	12	US-09-962-055-11	Sequence 31, App1
14	54	100.0	78	9	US-09-976-740-31	Sequence 31, App1
15	54	100.0	78	13	US-10-671-242-31	Sequence 31, App1
16	54	100.0	78	13	US-10-023-529-31	Sequence 31, App1
17	54	100.0	78	15	US-10-023-523-31	Sequence 31, App1
18	54	100.0	78	15	US-10-616-187-31	Sequence 31, App1
19	54	100.0	84	9	US-09-962-055-37	Sequence 37, App1
20	54	100.0	84	9	US-09-976-740-37	Sequence 37, App1
21	54	100.0	84	12	US-10-671-242-37	Sequence 37, App1
22	54	100.0	84	13	US-10-023-529-37	Sequence 37, App1
23	54	100.0	84	13	US-10-023-523-37	Sequence 37, App1
24	54	100.0	84	15	US-10-671-242-37	Sequence 37, App1
25	54	100.0	1208	15	US-09-962-055-16	Sequence 16, App1
26	54	100.0	1208	9	US-09-976-740-16	Sequence 16, App1
27	54	100.0	1208	12	US-10-671-242-16	Sequence 16, App1
28	54	100.0	1208	13	US-10-023-529-16	Sequence 16, App1
29	54	100.0	1208	13	US-10-023-523-16	Sequence 16, App1
30	54	100.0	1208	15	US-10-616-187-16	Sequence 16, App1
31	54	100.0	1336	14	US-10-102-806-247	Sequence 247, App
32	54	100.0	1362	9	US-09-962-055-12	Sequence 12, App1
33	54	100.0	1362	9	US-09-976-740-12	Sequence 12, App1
34	54	100.0	1362	12	US-10-671-242-12	Sequence 12, App1
35	54	100.0	1362	13	US-10-023-529-12	Sequence 12, App1
36	54	100.0	1362	13	US-10-023-523-12	Sequence 12, App1
37	54	100.0	1362	15	US-10-616-187-12	Sequence 12, App1
38	54	100.0	1422	9	US-09-962-055-13	Sequence 13, App1
39	54	100.0	1422	9	US-09-976-740-13	Sequence 13, App1
40	54	100.0	1422	12	US-10-671-242-13	Sequence 13, App1
41	54	100.0	1422	13	US-10-023-529-13	Sequence 13, App1
42	54	100.0	1422	13	US-10-023-523-13	Sequence 13, App1
43	54	100.0	1422	15	US-10-616-187-13	Sequence 13, App1
44	54	100.0	1445	15	US-09-945-527-6	Sequence 6, App1
45	54	100.0	1614	9	US-09-976-740-45	Sequence 45, App1

ALIGNMENTS

RESULT 1
US-09-962-055-32
; Sequence 32, Application US/09962055
; Patent No. US2002005203A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Arjona, Anibal A.
;   Law, Simon W.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804

; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS

Result No.   Score   Query   Match Length   DB   ID   Description
----------   -----   -----   ----- ------   --   --   -----------
                               %

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/962,055
  FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/979,608
  FILING DATE: 26-Nov-1997
  APPLICATION NUMBER: US 60/031,930
  FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Myers, Louis
  REGISTRATION NUMBER: 35,965
  REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
  LENGTH: 33 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
FEATURE:
  NAME/KEY: Coding Sequence
  LOCATION: 1...33
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-962-055-32

Alignment Scores:
Pred. No.:
Score: 0.00499   Length: 33
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                       Gaps: 0

US-09-962-055-32:

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db   1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

US-09-976-740-21 (1-11) x US-09-962-055-32 (1-33)

RESULT 2
US-09-976-740-32
Sequence 32, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 33
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-32

Alignment Scores:
Pred. No.:
Score: 0.00499   Length: 33
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                       Gaps: 0

US-10-671-242-32

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db   1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33

US-09-976-740-21 (1-11) x US-09-976-740-32 (1-33)

RESULT 3
US-10-671-242-32
Sequence 32, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 33
TYPE: DNA
ORGANISM: Homo sapiens
US-10-671-242-32

Alignment Scores:
Pred. No.:
Score: 0.00499   Length: 33
Percent Similarity: 54.00   Matches: 11
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 12   Indels: 0
                                       Gaps: 0

US-09-976-740-21 (1-11) x US-10-671-242-32 (1-33)

RESULT 4
US-10-023-529-32
Sequence 32, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS

```
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 2001-12-17
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;
;  SEQ ID NO 32
;  LENGTH: 33
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-023-529-32

Alignment Scores:
Pred. No.:                              0.00499
Score:                                  54.00
Percent Similarity:                     100.00%
Best Local Similarity:                  100.00%
Query Match:                            13

US-09-976-740-21 (1-11) x US-10-023-529-32 (1-33)

Qy       1 ValSerGluGlySerGluValProGluSerAsp 11
           |||||||||||||||||||||||||||||||||
Db       1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33


RESULT 5
US-10-023-523-32
; Sequence 32, Application US/10023523
; Publication No.US20020152485A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,523
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 32
;  LENGTH: 33
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-023-523-32
```

```
Query Match:                            100.00%     Indels:      0
DB:                                     13           Gaps:        0

US-09-976-740-21 (1-11) x US-10-023-523-32 (1-33)

Qy       1 ValSerGluGlySerGluValProGluSerAsp 11
           |||||||||||||||||||||||||||||||||
Db       1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33


RESULT 6
US-10-616-187-32
; Sequence 32, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/616,187
;  CURRENT FILING DATE: 2003-07-09
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 32
;  LENGTH: 33
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-616-187-32

Alignment Scores:
Pred. No.:                              0.00499
Score:                                  54.00
Percent Similarity:                     100.00%
Best Local Similarity:                  100.00%
Query Match:                            15

US-09-976-740-21 (1-11) x US-10-616-187-32 (1-33)

Qy       1 ValSerGluGlySerGluValProGluSerAsp 11
           |||||||||||||||||||||||||||||||||
Db       1 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 33


RESULT 7
US-09-962-055-38
; Sequence 38, Application US/09962055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;                      BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;                      TREATING ATHEROSCLEROSIS
;  NUMBER OF SEQUENCES: 42
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Fish & Richardson P.C.
;  STREET: 225 Franklin Street
```

Length: 33
Matches: 11
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-Nov-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..36
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-962-055-38

Alignment Scores:

Pred. No.:			
Score:	0.00543	Length:	36
Percent Similarity:	54.00	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	9	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x US-09-962-055-38 (1-36)

```
Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db  4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36
```

RESULT 8
US-09-976-740-38
Sequence 38, Application US/0997576740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 36
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-38

Alignment Scores:

Pred. No.:			
Score:	0.00543	Length:	36
Percent Similarity:	54.00	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	9	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x US-09-976-740-38 (1-36)

```
Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db  4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36
```

RESULT 9
US-10-671-242-38
Sequence 38, Application US/10671242
Publication No. US20040004941
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 38
LENGTH: 36
TYPE: DNA
ORGANISM: Homo sapiens
US-10-671-242-38

Alignment Scores:

Pred. No.:			
Score:	0.00543	Length:	36
Percent Similarity:	54.00	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	12	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x US-10-671-242-38 (1-36)

```
Qy  1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db  4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36
```

RESULT 10
US-10-023-529-38
Sequence 38, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.
; APPLICANT: Law, Simon W.
; APPLICANT: Lees, Robert S.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-38

Alignment Scores:
Pred. No.:
Score: 0.00543
Percent Similarity: 54.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13

Length: 36
Matches: 11
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-21 (1-11) x US-10-023-529-38 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db 4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 11
US-10-023-523-38
; Sequence 38, Application US/1002523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Law, Simon W.
; APPLICANT: Lees, Robert S.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: H

US-10-023-523-38
Alignment Scores:
Pred. No.:
Score: 0.00543
Percent Similarity: 54.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13

Length: 36
Matches: 11
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-21 (1-11) x US-10-023-523-38 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db 4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 12
US-10-616-187-38
; Sequence 38, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-187-38

Alignment Scores:
Pred. No.:
Score: 0.00543
Percent Similarity: 54.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 15

Length: 36
Matches: 11
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-21 (1-11) x US-10-616-187-38 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db 4 GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 36

RESULT 13
US-09-962-055-31
; Sequence 31, Application US/09962055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..78
SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-962-055-31

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11

Db   46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

US-09-976-740-21 (1-11) x US-09-962-055-31 (1-78)

SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-31

Alignment Scores:
Pred. No.:   0.0116
Score: 54.00   Length: 78
Percent Similarity: 100.00%   Matches: 11
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                               Gaps: 0

RESULT 14
US-09-976-740-31
Sequence 31, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-31

Alignment Scores:
Pred. No.:   0.0116
Score: 54.00   Length: 78
Percent Similarity: 100.00%   Matches: 11
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                               Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
Db   46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78

US-09-976-740-21 (1-11) x US-09-976-740-31 (1-78)

RESULT 15
US-10-671-242-31
Sequence 31, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-10-671-242-31

Alignment Scores:
Pred. No.:   0.0116
Score: 54.00   Length: 78
Percent Similarity: 100.00%   Matches: 11
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 12   Indels: 0
                               Gaps: 0

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||
US-09-976-740-21 (1-11) x US-10-671-242-31 (1-78)

Db   46 GTGTCAGAGGGGCCTCTTGAAGTGCCCGAGAGTGAC 78

Search completed: March 13, 2004, 04:26:14
Job time : 15.9143 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:       March 12, 2004, 19:55:37 ; Search time 166.319 Seconds
                                         (without alignments)
                                         1975.018 Million cell updates/sec

Title:          US-09-976-740-21
Perfect score:  54
Sequence:       1 VSEGSEVPESD 11

Scoring table:  BLOSUM62
                Xgapop  10.0  , Xgapext  0.5
                Ygapop  10.0  , Ygapext  0.5
                Fgapop   6.0  , Fgapext  7.0
                Delop    6.0  , Delext   7.0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched:       27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:      5026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame_plus_p2n.model  /DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -OFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1_10232_@runat_10032004_094548_19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
             1: em_estba:*
             2: em_esthum:*
             3: em_estin:*
             4: em_estou:*
             5: em_estmu:*
             6: em_estov:*
             7: em_estpl:*
             8: em_estro:*
             9: em_htc:*
            10: gb_est1:*
            11: gb_est2:*
            12: gb_est3:*
            13: gb_est4:*
            14: gb_est5:*
            15: em_estfun:*
            16: em_estom:*
            17: em_gss_hum:*
            18: em_gss_inv:*
            19: em_gss_pln:*
            20: em_gss_vrt:*
            21: em_gss_fun:*
            22: em_gss_mam:*
            23: em_gss_mus:*
            24: em_gss_pro:*
            25: em_gss_rod:*
            26: em_gss_png:*
            27: em_gss_vr1:*
            28: gb_gssI:*
            29: gb_gss2:*
```

```
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result        %
No.  Score  Query  Match  Length  DB  ID          Description
            ----------------------------------------------------------------
  1   54   100.0   100.0   222    9  AA807020    AA807020 oc30g04.s
  2   54   100.0   100.0   253    9  AI713567    AI713567 UI-R-AG1-
  3   54   100.0   100.0   269    9  AA029068    AA029068 zk09h07.s
  4   54   100.0   100.0   271   12  AA765474    AA765474 oa03d01.s
  5   54   100.0   100.0   274    9  BI004562    BI004562 MR4-HN005
  6   54   100.0   100.0   275    9  AA806888    AA806888 oc32g06.s
  7   54   100.0   100.0   278    9  AA810871    AA810871 ob64g05.s
  8   54   100.0   100.0   284    9  AA766034    AA766034 oa15b09.s
  9   54   100.0   100.0   289    9  AA804533    AA804533 ns28c06.s
 10   54   100.0   100.0   302   10  AI137809    AI137809 UI-R-C0-h
 11   54   100.0   100.0   302    9  BF194967    BF194967 7o91b05.x
 12   54   100.0   100.0   322    9  AI470106    AI470106 tj90g09.x
 13   54   100.0   100.0   324   10  BF806978    BF806978 QV4-CI015
 14   54   100.0   100.0   325   10  BE100055    BE100055 UI-R-BJ1-
 15   54   100.0   100.0   325   10  BE112745    BE112745 UI-R-BJ1-
 16   54   100.0   100.0   328   10  BF561482    BF561482 UI-R-C0-h
 17   54   100.0   100.0   340    9  AI711065    AI711065 UI-R-AE1-
 18   54   100.0   100.0   342   10  AI172508    AI172508 UI-R-C2p-
 19   54   100.0   100.0   345   10  BF941758    BF941758 nad92h03.
 20   54   100.0   100.0   348    9  AI548990    AI548990 UI-R-C3-t
 21   54   100.0   100.0   349   10  BE114632    BE114632 UI-R-BJ1-
 22   54   100.0   100.0   367    9  AA769505    AA769505 nz35b01.s
 23   54   100.0   100.0   375    9  AA649303    AA649303 ns31g12.s
 24   54   100.0   100.0   383   10  AW845391    AW845391 CM4-CT004
 25   54   100.0   100.0   384    9  AA836383    AA836383 oa24d07.s
 26   54   100.0   100.0   386    9  AA766164    AA766164 oa24a07.s
 27   54   100.0   100.0   395   10  BE111716    BE111716 UI-R-BJ1-
 28   54   100.0   100.0   397   10  AW594381    AW594381 hg66e08.x
 29   54   100.0   100.0   406    9  AI230441    AI230441 EST227136
 30   54   100.0   100.0   406   10  AI230496    AI230496 EST227191
 31   54   100.0   100.0   412   10  AW134620    AW134620 UI-M-BH3-
 32   54   100.0   100.0   424   10  BF470100    BF470100 UI-M-BH3-
 33   54   100.0   100.0   428    9  AA944363    AA944363 EST199862
 34   54   100.0   100.0   429    9  AI097526    AI097526 qb87g10.x
 35   54   100.0   100.0   430    9  AI548989    AI548989 UI-R-C3-t
 36   54   100.0   100.0   430   10  AW142485    AW142485 EST292737
 37   54   100.0   100.0   436   10  AI556877    AI556877 UI-R-C2p-
 38   54   100.0   100.0   436    9  AW490346    AW490346 UI-M-BH3-
 39   54   100.0   100.0   439    9  AI102597    AI102597 EST211886
 40   54   100.0   100.0   446    9  AI379283    AI379283 tc73b06.x
 41   54   100.0   100.0   451    9  AW016794    AW016794 UI-H-BI0p
 42   54   100.0   100.0   453   10  AW531666    AW531666 UI-R-C4-a
 43   54   100.0   100.0   453   10  BE199810    BE199810 ug71b07.x
 44   54   100.0   100.0   455    9  AA827627    AA827627 od55f01.s
 45   54   100.0   100.0   455    9  AI186973    AI186973 qe28f06.x
```

```
                              ALIGNMENTS

RESULT 1
AA807020
AA807020       AA807020        222 bp     mRNA        linear      EST 07-APR-1998
LOCUS          oc30g04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351254 3'
DEFINITION     similar to contains element MSR1 repetitive element ;, mRNA
               sequence.
ACCESSION      AA807020
VERSION        AA807020.1  GI:2876596
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

Column 1

```
REFERENCE   1 (bases 1 to 222)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1153    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 211.
FEATURES            Location/Qualifiers
     source         1..222
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:1351254"
                    /tissue_type="germinal center B cell"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_GCB1"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                    was prepared from human tonsillar cells enriched for
                    germinal center B cells by flow sorting (CD20+, IgD-),
                    provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                    (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                    primed with a Not I - oligo(dT) primer
                    [5'-TGTTACCAATCTGAAGTGGGAGGCGGCCGCCCTCTATTTTTTTTTTTTTTTTTT-3'
                    ]. Double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not I
                    and Eco RI sites of the modified pT7T3 vector. Library
                    went through one round of normalization, and was
                    constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN

Alignment Scores:
Pred. No.:               3.37         Length:       222
Score:                  54.00         Matches:       11
Percent Similarity:    100.00%        Conservative:   0
Best Local Similarity: 100.00%        Mismatches:     0
Query Match:           100.00%        Indels:         0
DB:                      9            Gaps:           0

US-09-976-740-21 (1-11) x AA807020 (1-222)

Qy     1 ValSerGlyGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||||||||
Db   124 GTGTCAGGAGGGCTCTGAAGTGCCGGAGAGTGAC 156

REFERENCE   1 (bases 1 to 253)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
```

Column 2

```
JOURNAL     discovery
            Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Oligo-dT track not found. Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Clones will be available through
            Research Genetics (www.resgen.com) The following repetitive
            elements were found in this cDNA sequence: 93-134,
            >GC_rich#Low complexity 135-216, >(GGA)n#Simple_repeat
            POLYA=No.
FEATURES            Location/Qualifiers
     source         1..253
                    /organism="Rattus norvegicus"
                    /mol_type="mRNA"
                    /strain="Sprague-Dawley"
                    /db_xref="taxon:10116"
                    /clone="UI-R-AG1-aan-a-08-0-UI"
                    /clone_lib="UI-R-AG1"
                    /lab_host="DH10B"
                    /dev_stage="adult"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-AG1
                    library is a normalized library constructed from 13 dpc
                    rat ventricle. The tag is a string of 6 nucleotides
                    present between the Not I site and the oligo-dT track.
                    The library was constructed as described by Bonaldo,
                    Lennon and Soares, Genome Research 6: 791-806, 1996.
                    Tissue provided by Jim Lin, Department of Biology,
                    University of Iowa.
                    TAG TISSUB=atrium at 16.5 dpc
                    TAG_LIB=UI-R-AG1
                    TAG_SEQ=GATTC"
ORIGIN

US-09-976-740-21 (1-11) x AI713567 (1-253)

Qy     1 ValSerGlyGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||||||||
Db   221 GTATCTGAGGGCTCGGAAGTGCCGGAGAGTGAC 253

RESULT 2
LOCUS       AI713567   253 bp   mRNA   linear   EST 08-JUN-1999
DEFINITION  UI-R-AG1-aan-a-08-0-UI.s1 UI-R-AG1 Rattus norvegicus cDNA clone
            UI-R-AG1-aan-a-08-0-UI 3', mRNA sequence.
ACCESSION   AI713567
VERSION     AI713567.1  GI:5017367
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 269)
```

Column 3

```
Alignment Scores:
Pred. No.:               3.98         Length:       253
Score:                  54.00         Matches:       11
Percent Similarity:    100.00%        Conservative:   0
Best Local Similarity: 100.00%        Mismatches:     0
Query Match:           100.00%        Indels:         0
DB:                      9            Gaps:           0

RESULT 3
LOCUS       AA029068 .   269 bp   mRNA   linear   EST 09-MAY-1997
DEFINITION  zk09h07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
            IMAGE:470077 3', mRNA sequence.
ACCESSION   AA029068
VERSION     AA029068.1  GI:1496470
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 269)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
```

Column 1

AUTHORS   Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
          Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
          Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
          and Marra,M.
TITLE   Generation and analysis of 280,000 human expressed sequence tags
JOURNAL   Genome Res. 6 (9), 807-828 (1996)
MEDLINE   97044478
PUBMED   8889549
COMMENT   Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Possible reversed clone: polyT not found
          Possible reversed clone: polyT not found
          IMAGE Consortium (info@image.llnl.gov)
          Insert Length: 1135   Std Error: 0.00
          Seq primer: -40M13 fwd. from Amersham
          High quality sequence stop: 229.

FEATURES   Location/Qualifiers
     source   1..269
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:375607"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:470077"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;
                     Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     AACTGGAAGAATTCGGCGGCCGCCCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization.
                     constructed by M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:   4.3   Length: 269
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 9   Indels: 0
                                     Gaps: 0
DB:

US-09-976-740-21 (1-11) x AA029068 (1-269)

Qy   1 ValSerGlyGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db 169 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 201

RESULT 4
LOCUS   AA765474   271 bp   mRNA   linear   EST 08-FEB-1998
DEFINITION oa03d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303873 3'
            similar to contains Alu repetitive element;,contains element MER22
            repetitive element;, mRNA sequence.
ACCESSION   AA765474
VERSION   AA765474.1 GI:2816712
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 271)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index

Column 2

JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
          Ph.D., Gerald Marti, M.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Insert Length: 1136   Std Error: 0.00
          Seq primer: -40m13 fwd. ET from Amersham
          High quality sequence stop: 269.

FEATURES   Location/Qualifiers
     source   1..271
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1303873"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGCGGCCGCCCTCATTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:   4.34   Length: 271
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 9   Indels: 0
                                     Gaps: 0
DB:

US-09-976-740-21 (1-11) x AA765474 (1-271)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
       |||||||||||||||||||||||||||||||||
Db 127 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 159

RESULT 5
LOCUS   BI004562   274 bp   mRNA   linear   EST 13-JUN-2001
DEFINITION MR4-HN0054-070301-002-g04 HN0054 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI004562
VERSION   BI004562.1 GI:14408636
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 274)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml12.pl?t1=MR4&t2=MR4-HN0054-
070301-002-g04&t3=2001-03-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 39
High quality sequence stop: 274.

FEATURES
　　source　　1..274
　　　　/organism="Homo sapiens"
　　　　/mol_type="mRNA"
　　　　/db_xref="taxon:9606"
　　　　/dev_stage="Adult"
　　　　/clone_lib="HN0054"
　　　　/note="Organ: head, normal; Vector: puc18; Site_1: SmaI;
　　　　Site_2: SmaI; A mini-library was made by cloning products
　　　　derived from ORESTES PCR (U.S. Letters Patent application
　　　　No. 196,716 - Ludwig Institute for Cancer Research)
　　　　profiles into the pUC 18 vector. Reverse transcription of
　　　　tissue mRNA and cDNA amplification were performed under
　　　　low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.:　　4.4　　　　　　Length:　　274
Score:　　54.00　　　　　　Matches:　　11
Percent Similarity:　100.00%　　Conservative:　0
Best Local Similarity:　100.00%　　Mismatches:　0
Query Match:　12　　　　　Indels:　0
DB:　　　　　　　　　　Gaps:　0

US-09-976-740-21 (1-11) x BI004562 (1-274)

Qy　1 ValSerGlyGlySerGluValProGluSerAsp 11
　　　||||||||||||||||||||||||||||||||||
Db　206 GTGTCAGAGGGGCTCTGAAGTGCCCGAGAGTGAC 174

RESULT 6
LOCUS　AA806888　　275 bp　　mRNA　　linear　EST 07-APR-1998
DEFINITION cc32g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351450 3',
similar to contains element TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AA806888
VERSION AA806888.1　GI:2876464
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 275)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1112　Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 229.

FEATURES
　　source　　1..275
　　　　/organism="Homo sapiens"
　　　　/mol_type="mRNA"
　　　　/db_xref="taxon:9606"
　　　　/clone="IMAGE:1351450"
　　　　/tissue_type="germinal center B cell"
　　　　/clone_lib="NCI_CGAP_GCB1"
　　　　/lab_host="DH10B"
　　　　/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
　　　　polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
　　　　was prepared from human tonsillar cells enriched for
　　　　germinal center B cells by flow sorting (CD20+, IgD-),
　　　　provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
　　　　(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
　　　　primed with a Not I - oligo(dT) primer
　　　　[5'-TGTTACCAATCTGAAGTGGGGCGGGCGCGGCCGCTCAATTTTTTTTTTTTTTTTT-3',
　　　　]. Double-stranded cDNA was ligated to Eco RI adaptors
　　　　(Pharmacia), digested with Not I and cloned into the Not I
　　　　and Eco RI sites of the modified pT7T3 vector. Library
　　　　went through one round of normalization, and was
　　　　constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:　　4.42　　　　　Length:　　275
Score:　　54.00　　　　　　Matches:　　11
Percent Similarity:　100.00%　　Conservative:　0
Best Local Similarity:　100.00%　　Mismatches:　0
Query Match:　9　　　　　Indels:　0
DB:　　　　　　　　　　Gaps:　0

US-09-976-740-21 (1-11) x AA806888 (1-275)

Qy　1 ValSerGlyGlySerGluValProGluSerAsp 11
　　　|||||||||||||||||||||||||||||||
Db　130 GTGTCAGAGGGGCTCTGAAGTGCCCGAGAGTGAC 162

RESULT 7
LOCUS　AA810871　　278 bp　　mRNA　　linear　EST 19-FEB-1998
DEFINITION ob64g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336184 3',
similar to contains element PTR7 repetitive element ;, mRNA
sequence.
ACCESSION AA810871
VERSION AA810871.1　GI:2880482
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 278)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES
     source
High quality sequence stop: 269.
             Location/Qualifiers
             1..278
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:1336184"
             /tissue_type="germinal center B cell"
             /lab_host="DH10B"
             /clone_lib="NCI_CGAP_GCB1"
             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
             polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
             was prepared from human tonsillar cells enriched for
             germinal center B cells by flow sorting (CD20+, IgD-),
             provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
             (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
             primed with a Not I - oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGAGCCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'
             ]. Double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Not I and cloned into the Not I
             and Eco RI sites of the modified pT7T3 vector. Library
             went through one round of normalization, and was
             constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:   4.48
Score: 54.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

US-09-976-740-21 (1-11) x AA810871 (1-278)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||||
Db 127 GTGTCAGAGGGCCTCTGAAGTGCCCGAGAGTGAC 159

RESULT 8
AA766034
LOCUS   AA766034   284 bp   mRNA   linear   EST 08-FEB-1998
DEFINITION oa15b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1305017 3'
            similar to contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   AA766034
VERSION   AA766034.1 GI:2817272
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 284)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1100   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 269.

FEATURES
     source
High quality sequence stop: 283.
             Location/Qualifiers
             1..284
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:1305017"
             /tissue_type="germinal center B cell"
             /lab_host="DH10B"
             /clone_lib="NCI_CGAP_GCB1"
             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
             polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
             was prepared from human tonsillar cells enriched for
             germinal center B cells by flow sorting (CD20+, IgD-),
             provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
             (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
             primed with a Not I - oligo(dT) primer
             [5'-TGTTACCAATCTGAAGTGGAGCCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'
             ]. Double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Not I and cloned into the Not I
             and Eco RI sites of the modified pT7T3 vector. Library
             went through one round of normalization, and was
             constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.:   4.6
Score: 54.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

US-09-976-740-21 (1-11) x AA766034 (1-284)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
        |||||||||||||||||||||||||||||||||||
Db 126 GTGTCAGAGGGCCTCTGAAGTGCCCGAGAGTGAC 158

RESULT 9
AA804533
LOCUS   AA804533   289 bp   mRNA   linear   EST 18-FEB-1998
DEFINITION ns28c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184938 3'
            similar to contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION   AA804533
VERSION   AA804533.1 GI:2873664
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 289)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1490   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 271.

FEATURES
     source
             Location/Qualifiers
             1..289

RESULT 10

```
RESULT 10
Alignment Scores:
Pred. No.:          4.7
Score:              54.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:        100.00%
DB:                 9

ORIGIN

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||||||||
Db  87 GTGTCAGAGGGGCTCTGAAGTGCCCAGAGAGTGAC 119

US-09-976-740-21 (1-11) x AA804533 (1-289)

DB:                 9
Query Match:        100.00%        Gaps:        0
Best Local Similarity: 100.00%    Indels:      0
Percent Similarity: 100.00%       Mismatches:  0
Score:              54.00         Conservative: 0
                                  Matches:     289
                     Length:      289

VERSION     AI137809.1  GI:3638586
ACCESSION   AI137809
DEFINITION  UI-R-CO-hz-h-01-0-UI 3', mRNA sequence.
            UI-R-CO-hz-h-01-0-UI.s1 UI-R-CO Rattus
LOCUS       AI137809            302 bp    mRNA    linear    EST 05-JUL-1999
                                           norvegicus cDNA clone
```

EST.
KEYWORDS
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.

REFERENCE   1 (bases 1 to 302)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED   8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.
            Fatima Bonaldo. Ph.D. Clone distribution: clones will be available
            through Research Genetics This clone is also available through the
            I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
            ID-178042 The following repetitive elements were found in this
            cDNA sequence: 93-134, >GC_rich#low_complexity 135-216,
            >(GGA)#Simple repeat
            Seq primer: M13 Forward
            PolyA=No.

FEATURES   Location/Qualifiers
     source   1..302
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-CO-hz-h-01-0-UI"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="UI-R-CO"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary, and muscle. The UI-R-E1
                     library consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-CO) was
                     constructed as follows: PCR amplified cDNA inserts from
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles. The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-CO
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)."

RESULT 11

```
RESULT 11
Alignment Scores:
Pred. No.:          4.97
Score:              54.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:        100.00%
DB:                 9

ORIGIN

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||||||||
Db 221 GTATCTGAGGGGCTCCGGAAGTGCCCAGAGTGAC 253

US-09-976-740-21 (1-11) x AI137809 (1-302)

DB:                 9
Query Match:        100.00%        Gaps:        0
Best Local Similarity: 100.00%    Indels:      0
Percent Similarity: 100.00%       Mismatches:  0
Score:              54.00         Conservative: 0
                                  Matches:     11
                     Length:      302

DEFINITION  7o9ib05.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643712 3',
LOCUS       BF194967            302 bp    mRNA    linear    EST 03-NOV-2000
            similar to contains element TAR1 TAR1 repetitive element ;; mRNA
            sequence.
ACCESSION   BF194967
VERSION     BF194967.1   GI:11081346
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 302)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
```

FEATURES

source   Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov.

Location/Qualifiers
1. .302
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3643712"
/tissue_type="fibrochroma"
/clone_lib="NCI_CGAP_Ov18"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGGCGGCCGCGCCGACATTTTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	4.97		
Score:	54.00	Length:	302
Percent Similarity:	100.00%	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	10	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x BF194967 (1-302)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
     |||||||||||||||||||||||||||||||||
Db   213 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 245

RESULT 12
LOCUS   AI470106   322 bp   mRNA   linear   EST 14-APR-1999
DEFINITION   tj90g09.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone
IMAGE:2148832 3' similar to contains TAR1.b2 PTR5 repetitive
element //, mRNA sequence.
ACCESSION   AI470106
VERSION   AI470106.1   GI:4332196
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 322)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 387   Std Error: 0.00
Seq primer: -40UP from Gibco.
High quality sequence stop: 322.

FEATURES

source   Location/Qualifiers
1. .322
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2148832"
/lab_host="DH10B"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with

---

libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 322208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
752280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	5.39		
Score:	54.00	Length:	322
Percent Similarity:	100.00%	Matches:	11
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	9	Indels:	0
		Gaps:	0

US-09-976-740-21 (1-11) x AI470106 (1-322)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
     |||||||||||||||||||||||||||||||||
Db   197 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 229

RESULT 13
LOCUS   BF806978   324 bp   mRNA   linear   EST 12-JAN-2001
DEFINITION   QV4-CI0151-091100-522-a05 CI0151 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF806978
VERSION   BF806978.1   GI:12135967
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 324)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=QV4&t2-QV4-CI0151-
091100-522-a05&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 324.

FEATURES

source   Location/Qualifiers
1. .324
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

RESULT 14

```
BE100055     325 bp     mRNA     linear     EST 13-JUN-2000
UI-R-BJ1-atm-b-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-atm-b-09-0-UI 3', mRNA sequence.
```

LOCUS	BE100055
DEFINITION	UI-R-BJ1-atm-b-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
	UI-R-BJ1-atm-b-09-0-UI 3', mRNA sequence.
ACCESSION	BE100055
VERSION	BE100055.1 GI:8491941
KEYWORDS	EST.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 325)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
	discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB
	Coordinated Laboratory for Computational Genomics
	University of Iowa
	375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
	Tel: 319 335 8250
	Fax: 319 335 9565
	Email: bento-soares@uiowa.edu
	Oligo-dT track not found. Not I site shown in beginning of sequence
	is likely internal to the message. cDNA Library Preparation: M.B.
	Soares Lab Clone distribution: clones will be available through
	Research Genetics (www.resgen.com) The following repetitive
	elements were found in this cDNA sequence: 93-134,
	>GC_rich#Low complexity 135-216, >(GGA)n#Simple_repeat
	Seq primer: M13 Forward
	PolyA=No.

FEATURES   Location/Qualifiers
     source   1..325
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BJ1-atm-b-09-0-UI"
                     /clone_lib="UI-R-BJ1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
                     library is a subtracted library derived from the following
                     tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV

US-09-976-740-21 (1-11) x BE100055 (1-324)

Qy   1 ValSerGluGlyGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||||
Db   92 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 124
```

Alignment Scores:

Pred. No.:	
Score:	5.43
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10

Length:	324	Matches:	11
		Conservative:	0
		Mismatches:	0
		Indels:	0
		Gaps:	0

```
ORIGIN
/dev stage="Adult"
/clone_lib="CI0151"
/note="Organ: colon; ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716. - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
```

RESULT 15

```
BE112745     325 bp     mRNA     linear     EST 13-JUN-2000
UI-R-BJ1-avo-c-12-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-avo-c-12-0-UI 3', mRNA sequence.
```

LOCUS	BE112745
DEFINITION	UI-R-BJ1-avo-c-12-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
	UI-R-BJ1-avo-c-12-0-UI 3', mRNA sequence.
ACCESSION	BE112745
VERSION	BE112745.1 GI:8504850
KEYWORDS	EST.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 325)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
	discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB
	Coordinated Laboratory for Computational Genomics
	University of Iowa
	375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
	Tel: 319 335 8250
	Fax: 319 335 9565
	Email: bento-soares@uiowa.edu
	Oligo-dT track not found. Not I site shown in beginning of sequence
	is likely internal to the message. cDNA Library Preparation: M.B.
	Soares Lab Clone distribution: clones will be available through
	Research Genetics (www.resgen.com) The following repetitive
	elements were found in this cDNA sequence: 93-134,
	>GC_rich#Low complexity 135-216, >(GGA)n#Simple_repeat
	Seq primer: M13 Forward
	PolyA=No.

FEATURES   Location/Qualifiers
     source   1..325
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BJ1-avo-c-12-0-UI"
                     /clone_lib="UI-R-BJ1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
                     library is a subtracted library derived from the following
                     tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
                     canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,

US-09-976-740-21 (1-11) x BE100055 (1-325)

Qy   1 ValSerGluGlyGlySerGluValProGluSerAsp 11
              |||||||||||||||||||||||||||||||||||
Db   221 GTATCTGAGGGCTCGGAAGTGCCCGAGAGTGAC 253
```

**Alignment Scores:**

| | |
|---|---|
| Pred. No.: | |
| Score: | 5.45 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 10 |

| | | | |
|---|---|---|---|
| Length: | 325 | Matches: | 11 |
| | | Conservative: | 0 |
| | | Mismatches: | 0 |
| | | Indels: | 0 |
| | | Gaps: | 0 |

```
ORIGIN
AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
TAG_SEQ=None found"
```

ORIGIN

AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_SEQ=None found"

Alignment Scores:
Pred. No.:   5.45   Length: 325
Score: 54.00   Matches: 11
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 10   Gaps: 0

US-09-976-740-21 (1-11) x BE112745 (1-325)

Qy   1 ValSerGluGlySerGluValProGluSerAsp 11
         |||||||||||||||||||||||||||||||||
Db   221 GTATCTGAGGGGCTCGGAAGTGCCCGAGAGTGAC 253

Search completed: March 13, 2004, 04:01:41
Job time : 171.319 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:49:56 ; Search time 151.885 Seconds
(without alignments)
2853.675 Million cell updates/sec

Title: US-09-976-740-22
Perfect score: 58
Sequence: 1 EDDDPDGFLG 10

Scoring table: US-09-976-740-22

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US0997674O/runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US0997674O_@CGN_1_1_9705_@runat_10032004_094548_19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: gb_fun:*
17: gb_hum:*
18: gb_in:*
19: gb_mu:*
20: gb_om:*
21: gb_or:*
22: gb_ov:*
23: gb_pat:*
24: gb_ph:*
25: gb_pl:*
26: gb_ro:*
27: gb_sts:*
28: gb_un:*
29: em_vi:*
30: em_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	30	6	AR199541	AR199541 Sequence
2	58	100.0	30	6	AR374693	AR374693 Sequence
3	58	100.0	30	6	AR409328	AR409328 Sequence
4	58	100.0	30	6	AX235590	AX235590 Sequence
5	58	100.0	30	6	BD056455	BD056455 Novel low
6	58	100.0	425	6	AR418294	AR418294 Sequence
7	58	100.0	425	9	BD113847	BD113847 EST and e
8	58	100.0	982	9	BC007384	BC007384 Homo sapi
9	58	100.0	1134	9	BD275342	BD275342 49 Human
10	58	100.0	1208	6	AR199535	AR199535 Sequence
11	58	100.0	1208	6	AR374687	AR374687 Sequence
12	58	100.0	1208	6	AR409322	AR409322 Sequence
13	58	100.0	1208	6	AX239573	AX239573 Sequence
14	58	100.0	1208	6	BD056449	BD056449 Novel low
15	58	100.0	1470	9	BC030129	BC030129 Homo sapi
16	58	100.0	1614	9	AR409337	AR409337 Sequence
17	58	100.0	1614	9	AX239602	AX239602 Sequence
18	58	100.0	1617	9	AY453840	AY453840 Sequence
19	58	100.0	12425	9	AR409341	AR409341 Sequence
20	58	100.0	12425	9	AX239607	AX239607 Sequence
21	58	100.0	215265	9	AC134005	AC134005 Rattus no
22	58	100.0	237931	2	AC022098	AC022098 Homo sapi
23	58	100.0	279020	2	AC133803	AC133803 Rattus no
24	54	93.1	1362	6	AR199531	AR199531 Sequence
25	54	93.1	1362	6	AR374683	AR374683 Sequence
26	54	93.1	1362	6	AR409318	AR409318 Sequence
27	54	93.1	1362	6	AX239569	AX239569 Sequence
28	54	93.1	1362	6	BD056445	BD056445 Novel low
29	54	93.1	1422	6	AR199532	AR199532 Sequence
30	54	93.1	1422	6	AR374684	AR374684 Sequence
31	54	93.1	1422	6	AR409319	AR409319 Sequence
32	54	93.1	1422	6	AX239570	AX239570 Sequence
33	54	93.1	1422	6	BD056446	BD056446 Novel low
34	54	93.1	1617	6	AR199530	AR199530 Sequence
35	54	93.1	1617	6	AR374682	AR374682 Sequence
36	54	93.1	1617	6	AR409317	AR409317 Sequence
37	54	93.1	1617	6	AX239568	AX239568 Sequence
38	54	93.1	1617	6	BD056444	BD056444 Novel low
39	54	93.1	2560	4	AY453841	AY453841 Oryctolag
40	54	93.1	2561	6	AR409339	AR409339 Sequence
41	54	93.1	2561	6	AX239605	AX239605 Sequence
42	52	89.7	140795	2	AC079562	AC079562 Sequence
43	52	89.7	218687	2	AC079501	AC079501 Sequence
44	47	81.0	1376	8	AK063989	AK063989 Oryza sat
45	47	81.0	2291	8	AK102006	AK102006 Oryza sat

RESULT 1 ALIGNMENTS

```
LOCUS       AR199541      30 bp    DNA    linear   PAT 20-APR-2002
DEFINITION  Sequence 33 from patent US 6355451.
ACCESSION   AR199541
VERSION     AR199541.1  GI:20249615
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 33 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Qy          1 GluAspAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||
Db          1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x AR199541 (1-30)

Alignment Scores:
  Pred. No.:                          Length:        30
  Score:                 0.0138       Matches:       10
  Percent Similarity:    58.00        Conservative:  0
  Best Local Similarity: 100.00%      Mismatches:    0
  Percent Similarity:    100.00%      Indels:        0
  Best Local Similarity: 100.00%      Gaps:          0
  Query Match:           6
  DB:

RESULT 2
LOCUS       AR374693      30 bp    DNA    linear   PAT 18-DEC-2003
DEFINITION  Sequence 33 from patent US 6605588.
ACCESSION   AR374693
VERSION     AR374693.1  GI:40077508
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 33 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Qy          1 GluAspAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||
Db          1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x AR374693 (1-30)

Alignment Scores:
  Pred. No.:                          Length:        30
  Score:                 0.0138       Matches:       10
  Percent Similarity:    58.00        Conservative:  0
  Best Local Similarity: 100.00%      Mismatches:    0
  Percent Similarity:    100.00%      Indels:        0
  Best Local Similarity: 100.00%      Gaps:          0
  Query Match:           6
  DB:

RESULT 3
LOCUS       AR409328
DEFINITION  Sequence 33 from patent US 6632923.
ACCESSION   AR409328
VERSION     AR409328.1  GI:40160116
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 33 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Qy          1 GluAspAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||
Db          1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x AR409328 (1-30)

Alignment Scores:
  Pred. No.:                          Length:        30
  Score:                 0.0138       Matches:       10
  Percent Similarity:    58.00        Conservative:  0
  Best Local Similarity: 100.00%      Mismatches:    0
  Percent Similarity:    100.00%      Indels:        0
  Best Local Similarity: 100.00%      Gaps:          0
  Query Match:           6
  DB:

RESULT 4
LOCUS       AX239590      30 bp    DNA    linear   PAT 26-SEP-2001
DEFINITION  Sequence 33 from patent WO0164874.
ACCESSION   AX239590
VERSION     AX239590.1  GI:15797266
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 33 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Qy          1 GluAspAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||
Db          1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x AX239590 (1-30)

Alignment Scores:
  Pred. No.:                          Length:        30
  Score:                 0.0138       Matches:       10
  Percent Similarity:    58.00        Conservative:  0
  Best Local Similarity: 100.00%      Mismatches:    0
  Percent Similarity:    100.00%      Indels:        0
  Best Local Similarity: 100.00%      Gaps:          0
  Query Match:           6
  DB:

RESULT 5
LOCUS       BD056455
DEFINITION  Novel low density lipoprotein binding proteins and their use in
```

Left column

diagnosing and treating atherosclerosis,.

ACCESSION   BD056455
VERSION   BD056455.1 GI:22602061
KEYWORDS   JP 2001506983-A/13.
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 30)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 13 29-MAY-2001;
            BOSTON HEART FOUNDATION INC
COMMENT   PN   JP 2001506983-A/13
            PD   29-MAY-2001
            PF   26-NOV-1997 JP 199524870
            PR   27-NOV-1996 US 60/031930, 03-JUN-1997 US   60/048547 PI
            ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
            A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
            C07H21/00,
            C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
            Strandedness: Single;
            Topology: Linear;
  CC
  FH Key   Location/Qualifiers
FEATURES   source   Location/Qualifiers
            1..30
            /organism="Aequorea victoria"
            /mol_type="genomic DNA"
            /db_xref="taxon:6100"
ORIGIN

US-09-976-740-22 (1-10) x BD056455 (1-30)

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||||
Db   1 GAGGATGATGACCCCGATGGCTTCTTAGGG 30

Alignment Scores:
Pred. No.:
Score: 0.0138   Length: 30
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

RESULT 6
AR418294
LOCUS   AR418294   425 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 9791 from patent US 6639063.
ACCESSION   AR418294
VERSION   AR418294.1 GI:40173404
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 425)
  AUTHORS   Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
  TITLE   EST's and encoded human proteins
  JOURNAL   Patent: US 6639063-A 9791 28-OCT-2003;
FEATURES   source   Location/Qualifiers
            1..425
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||||
Db   1 GAGGATGATGACCCCGATGGCTTCTTAGGG 30

Right column

US-09-976-740-22 (1-10) x AR418294 (1-425)

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 200 GAGGATGATGACCCCGATGGCTTCTTAGGC 229

RESULT 7
BD113847
LOCUS   BD113847   425 bp   DNA   linear   PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION   BD113847
VERSION   BD113847.1 GI:23208751
KEYWORDS   JP 2002010789-A/5924.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 425)
  AUTHORS   Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
  TITLE   EST and encoded human protein.
  JOURNAL   Patent: JP 2002010789-A 5924 15-JAN-2002;
            GENSET CORP
COMMENT   OS   Homo sapiens (human)
            PN   JP 2002010789-A/5924
            PD   15-JAN-2002
            PF   07-AUG-2000 JP 2000280989
            PR   05-AUG-1999 US 60/147499
            PI   JEAN BAPTISTE DUMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE   PI
            GIORDANO
            PC   C12N15/09,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
            C12N1/21,
            PC   C12N15/10,C12P21/02,C12P21/08,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
FEATURES   source   Location/Qualifiers
            1..425
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
  FH Key   Location/Qualifiers
  FT source   1..425
                      /organism='Homo sapiens (human)'.
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.136   Length: 425
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

US-09-976-740-22 (1-10) x BD113847 (1-425)

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 200 GAGGATGATGACCCCGATGGCTTCTTAGGC 229

RESULT 8
BC007384
LOCUS   BC007384   982 bp   mRNA   linear   PRI 16-SEP-2003
DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
            IMAGE:3677194), partial cds.
ACCESSION   BC007384
VERSION   BC007384.2 GI:33988219
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 982)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

```
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   On Aug 20, 2003 this sequence version replaced gi:13938477.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
            clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 24 Row:g Column: 10.
FEATURES             Location/Qualifiers
     source          1..982
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677194"
                     /tissue_type="Lymph, Burkitt lymphoma"
                     /clone_lib="NIH_MGC_8"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            <1..982
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
     CDS             <1..711
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
                     /codon_start=1
                     /product="LOC90378 protein"
                     /protein_id="AAH07384.2"
                     /db_xref="GI:33988220"
                     /translation="PGRAPPAASARPSRSRKRGGGERVLKEKEEDEDEDEEEDDVSE
                     GSEVPESDRPAQAQHQLNGRRGPQSAKERVKEWTPCGPHQGGDSGRGPAPGSGTRQV
                     FSMAAMKEGGTASVATGPDSPSVPLPPGKPALPGADGFPGTFGFCPPGRKRKPSDPVEW
                     TWMDVVEYFTEAGFPPEQATAFQEEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHHI
                     KVLQQGHPEDDDPDGFG"
     misc_feature    469..669
                     /gene="LOC90378"
                     /note="SAM; Region: Sterile alpha motif. Widespread domain
```

in signalling and nuclear proteins. In EPH-related
tyrosine kinases, appears to mediate cell-cell initiated
signal transduction via the binding of SH2-containing
proteins to a conserved tyrosine that is phosphorylated.
In many cases mediates homodimerisation"
/db_xref="CDD:smart00454"

```
ORIGIN
```

US-09-976-740-22 (1-10) x BC007384 (1-982)

```
Qy          1 GluAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||||||||||
Db        679 GAGGATGATGACCCCGATGGCTTCTTAGGC 708
```

RSULT 9

LOCUS   BD275342/c   1134 bp   DNA   linear   PAT 17-JUL-2003
```
LOCUS       BD275342                      1134 bp    DNA        linear   PAT 17-JUL-2003
DEFINITION  49 Human Secreted Proteins.
ACCESSION   BD275342
VERSION     BD275342.1  GI:33085110
KEYWORDS    JP 2002539787-A/18.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1134)
  AUTHORS   Komatsoulis,G., Rosen,C.A. and Ruben,S.M.
  TITLE     49 Human Secreted Proteins
  JOURNAL   Patent: JP 2002539787-A 18 26-NOV-2002;
            Human Genome Sciences Inc
  COMMENT   OS  Homo sapiens
            PN  JP 2002539787-A/18
            PD  26-NOV-2002
            PF  16-MAR-2000 JP 2000606742
            PR  23-MAR-1999 US 60/126054,10-DEC-1999 US    60/169916 PI
            PR  23-MAR-1999 US 60/125054,10-DEC-1999 US
            George komatsoulis,craig a.rosen,steven m ruben CC
            FH  Key          Location/Qualifiers
FEATURES             Location/Qualifiers
     source          1..1134
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

US-09-976-740-22 (1-10) x BD275342 (1-1134)

```
Alignment Scores:
  Pred. No.:              0.317
  Score:                  58.00
  Percent Similarity:     100.00%    Conservative:    0
  Best Local Similarity:  100.00%    Mismatches:      0
  Query Match:            6          Indels:          0
  DB:                                Gaps:            0
```

RESULT 10

AR199535
```
LOCUS       AR199535                      1208 bp    DNA        linear   PAT 20-APR-2002
DEFINITION  Sequence 16 from patent US 6355451.
ACCESSION   AR199535
VERSION     AR199535.1  GI:20496609
KEYWORDS    .
```

```
Qy          1 GluAspAspProAspGlyPheLeuGly 10
              ||||||||||||||||||||||||||||||||||||||
Db        495 GAGGATGATGACCCCGATGGCTTCTTAGGC 466
```

ORIGIN

```
Alignment Scores:
  Pred. No.:              0.317
  Score:                  58.00
  Percent Similarity:     100.00%    Conservative:    0
  Best Local Similarity:  100.00%    Mismatches:      0
  Query Match:            6          Indels:          0
  DB:                                Gaps:            0
```

```
TITLE       Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   (bases 1 to 982)
```

```
  AUTHORS   Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
```

SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 16 12-MAR-2002;
FEATURES   Location/Qualifiers
  source   1..1208
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.335   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 GluAspAspAlaProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AR199535 (1-1208)

RESULT 11
LOCUS   AR374687   1208 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6605588.
ACCESSION   AR374687
VERSION   AR374687.1 GI:40077502
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 16 12-AUG-2003;
FEATURES   Location/Qualifiers
  source   1..1208
           /organism="unknown"
           /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.335   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 GluAspAspAlaProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AR374687 (1-1208)

RESULT 12
LOCUS   AR409322   1208 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6632923.
ACCESSION   AR409322
VERSION   AR409322.1 GI:40160110
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 16 14-OCT-2003;
FEATURES   Location/Qualifiers
  source   1..1208
           /organism="unknown"
           /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.335   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 GluAspAspAlaProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AR409322 (1-1208)

RESULT 13
LOCUS   AX239573   1208 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION Sequence 16 from Patent WO0164874.
ACCESSION   AX239573
VERSION   AX239573.1 GI:15797257
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 16 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
  source   1..1208
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
  CDS   <1..654
           /codon_start=1
           /note="unnamed protein product"
           /protein_id="CAC88296.1"
           /db_xref="GI:15799258"
           /db_xref="REMTREMBL:CAC88296"
           /translation="EERVLEKSEEEDDEDDEDEEDDVSEGSEVPESDRPAGAQHQLN
           GERGPQSAKERVKEWTPCGPHQGQDEGRGPAPGSSGTRQVFSMAAMNKEGGTRASVATGP
           DSPSPVFLPPGKPALPGADGPPGCPPGRKEKPSDSDPVEWTVNDVVEYFTEAGFPEQAT
           AFQEQEIDGKSLLLMQRTDVLTGLSRLGPALKIYEHHIKVLQQGHFEDDPDGFLG"

Alignment Scores:
Pred. No.:
Score: 0.335   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                       Gaps: 0

Qy   1 GluAspAspAlaProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AX239573 (1-1208)

```
BD056449
LOCUS       BD056449                1208 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis.
ACCESSION   BD056449
VERSION     BD056449.1  GI:22602055
KEYWORDS    JP 200150983-A/7.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 200150983-A 7 29-MAY-2001;
            BOSTON HEART FOUNDATION INC
COMMENT     PN   JP 200150983-A/7
            PD   29-MAY-2001
            PF   26-NOV-1997  JP 199824870
            PR   27-NOV-1996 US   60/031930,03-JUN-1997 US  60/048547 PI
            ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
            A61K38/04,A61K38/17,A61K3/00,A61K48/00,A61K49/00,A61K51/08, PC
            C07H21/00,
            PC   C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
            C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
            Strandedness: Single;
            Topology: Linear;
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
     FH   Key             Location/Qualifiers
ORIGIN
Alignment Scores:
Pred. No.:
Score:                  0.335
Percent Similarity:     58.00
Best Local Similarity:  100.00%
Query Match:            100.00%
DB:                     6

                        Length:       1208
                        Matches:        10
                        Conservative:    0
                        Mismatches:      0
                        Indels:          0
                        Gaps:            0

US-09-976-740-22 (1-10) x BD056449 (1-1208)

Qy     1 GluAspAlaAspproAspGlyPheLeuGly 10
           ||||||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

```
BC030129
LOCUS       BC030129                1470 bp    mRNA    linear   PRI 16-SEP-2003
DEFINITION  Homo sapiens hypothetical protein BC007784, mRNA (cDNA clone
            IMAGE:3943601), partial cds.
ACCESSION   BC030129
VERSION     BC030129.2  GI:33871478
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1470)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
```

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

```
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1470)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:22539615.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Tsurgeon,C.,
            Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 15 Row: m Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction.
FEATURES             Location/Qualifiers
     source          1..1470
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3943601"
                     /tissue_type="Lung, small cell carcinoma"
                     /clone_lib="NIH_MGC_7"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            1..1470
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
     CDS             <1..890
                     /gene="LOC90378"
                     /codon_start=3
                     /product="LOC90378 protein"
                     /protein_id="AAH30129.1"
                     /db_xref="GI:33871479"
                     /db_xref="LocusID:90378"
                     /translation="GAARPVSLREVVRYLGGSGGAGRLTRGRVQGLLEEBAAARGRL
                     ERPRLGALLALPRGDRPGRAPPAASARPSRSRKRGGEERVLEKEBEDDDEDEDDVS
                     EGBSVPESDRPAGAQHHQLNRGRGPQSAKERVREWTPCGFPHQGQDEGRPAPGSGTRQ
                     VFSMAAMKEGGTASVArGPDSPSPVPLPPGGKPALPGADGTPPGCPGGKKEPSDPVE
                     WTVMDVVEYFTEAGFPGQATAFQEQEIDGKSLILMQRTDVLTGLSIRLGPALKIYEHH
                     IKVLQGHFEDDDPDGFLG"
```

misc_feature   648..848
                /gene="LOC90378"
                /note="SAM; Region: Sterile alpha motif. Widespread domain
                in signalling and nuclear proteins. In EPH-related
                tyrosine kinases, appears to mediate cell-cell initiated
                signal transduction via the binding of SH2-containing
                proteins to a conserved tyrosine that is phosphorylated.
                In many cases mediates homodimerisation"
                /db_xref="CDD:smart00454"

ORIGIN

Alignment Scores:
Pred. No.:   0.397
Score: 58.00
Percent Similarity: 100.00%   Length: 1470
Best Local Similarity: 100.00%   Matches: 10
Query Match: 100.00%   Conservative: 0
DB: 9   Mismatches: 0
                                         Indels: 0
                                         Gaps: 0

US-09-976-740-22 (1-10) x BC030129 (1-1470)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
           ||||||||||||||||||||||||||||
Db   858 GAGGATGATGACCCCGATGGCTTCTTAGGC 887

Search completed: March 13, 2004, 00:35:27
Job time : 152.885 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:48:14 ; Search time 15.8507 Seconds
                                    2680.137 Million cell updates/sec

Title: US-09-976-740-22
Perfect score: 58
Sequence: 1 EDDDPDGPIG 10

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6477726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO_spool_p/US09976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740@CGN_1_1.1596 @runat_10032004_094547_19532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
    1: geneseqn1980s:*
    2: geneseqn1990s:*
    3: geneseqn2000s:*
    4: geneseqn2001bs:*
    5: geneseqn2001as:*
    6: geneseqn2002s:*
    7: geneseqn2002as:*
    8: geneseqn2003bs:*
    9: geneseqn2003cs:*
   10: geneseqn2004s:*

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	58	100.0	30	5	AAH26505	Aah26505 Low densi
	2	58	100.0	1134	5	AAC59574	Aac59574 Human sec
c	3	58	100.0	1208	2	AAV32838	Aav32838 Human low
	4	58	100.0	1208	5	AAH26494	Aah26494 Human low
	5	58	100.0	1336	3	AAF21860	Aaf21860 Human bre
	6	58	100.0	1614	5	AAH26499	Aah26499 Human low
	7	58	100.0	12425	5	AAH26495	Aah26495 Human low
	8	54	93.1	1362	5	AAH26489	Aah26489 Rabbit lo
	9	54	93.1	1422	2	AAH26490	Aah26490 Rabbit lo
	10	54	93.1	1617	2	AAV32835	Aav32835 Rabbit lo
	11	54	93.1	1617	5	AAH26488	Aah26488 Rabbit lo
	12	54	93.1	2561	5	AAH26500	Aah26500 Rabbit lo
	13	44	75.9	539	7	ABX57356	Abx57356 Arabidops
	14	44	75.9	2838	6	ABZ14501	Abz14501 Arabidops
	15	44	75.9	2838	4	ADA68111	Ada68111 Arabidops
	16	44	75.9	3125	4	AAI66059	Aai66059 Arabidops
	17	43	74.1	390	4	AAC02200	Aac02200 Human wit
	18	43	74.1	1495	5	ABL50160	Abl50160 Human sec
	19	43	74.1	3590	4	ABL24639	Abl24639 Human sec
	20	43	74.1	2415	4	ABZ26243	Abz26243 Drosophil
	21	43	74.1	6647	4	ABL24638	Abl24638 Drosophil
	22	42	72.4	1926	3	AAA40319	Aaa40319 S. olerac
	23	41	70.7	404	7	ABX53231	Abx53231 Bovine ES
	24	41	70.7	421	7	ABN75194	Abn75194 Human ORF
	25	41	70.7	442	6	AAK88442	Aak88442 Human dig
	26	41	70.7	442	8	AAS39543	Aas39543 CDNA enco
	27	41	70.7	442	8	ADB32269	Adb32269 Human nov
	28	41	70.7	1169	9	ADC03035	Adc03035 Human nov
	29	41	70.7	1406	9	ADD30425	Add30425 Plant yie
	30	41	70.7	1406	9	ADE31450	Ade31450 Plant yie
	31	41	70.7	1470	6	ABZ11247	Abz11247 Human pol
	32	41	70.7	1770	6	ABL05627	Abl05627 Drosophil
c	33	41	70.7	2000	7	ADA72766	Ada72766 Rice gene
c	34	41	70.7	2018	6	ABQ79395	Abq79395 Gab2 enco
c	35	41	70.7	2855	4	ABL05496	Abl05496 Drosophil
c	36	41	70.7	3095	2	AAQ38525	Aaq38525 Human CEN
c	37	41	70.7	3132	6	ABK46187	Abk46187 cDNA enco
c	38	41	70.7	3132	6	AAD50452	Aad50452 Human CEN
c	39	41	70.7	5788	4	ABL05626	Abl05626 Drosophil
c	40	41	70.7	6045	4	AAH18244	Aah18244 Human CDN
c	41	41	70.7	11774	4	AAK90413	Aak90413 Human dig
c	42	41	70.7	11774	4	AAK69391	Aak69391 Human imm
c	43	41	70.7	11774	5	AAS39969	Aas39969 Genomic s
c	44	41	70.7	11774	5	ADB32929	Adb32929 Human nov
c	45	41	70.7	61557	4	AAS59521	Aas59521 Propionib

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 1

```
AAH26505
ID   AAH26505           standard; DNA; 30 BP.
AC   AAH26505;
DT   12-NOV-2001  (first entry)
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
OS   Mammalia.
PN   WO200164874-A2.
PR   02-MAR-2000; 2000US-0051789.
PR   14-JUL-2000; 2000US-00612689.
PA   (BOST-) BOSTON HEART FOUND INC.
PI   Lees AM, Lees RS, Law SW, Arjona AA;
DR   WPI; 2001-565505/63.
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
```

ALIGNMENTS

XX
Disclosure; Page 9; 143pp; English.
XX
PS
CC The present sequence is that of a polynucleotide encoding a fragment of
CC novel low density lipoprotein binding proteins (LBPs) of the invention
CC (see AAB2797-820). LBPs are capable of binding to native and methylated
CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC LBPs and their fragments are claimed, as well as expression vectors,
CC cells and methods of producing the LBPs. Methods of determining if an
CC animal is at risk for atherosclerosis, methods for evaluating an agent
CC for use in treating atherosclerosis, and methods for treating a cell
CC having an abnormality in structure or metabolism of LBP are also claimed,
CC as are pharmaceutical compositions comprising an LBP polypeptide or
CC nucleic acid, and vaccine compositions
XX
SQ Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0025
Score: 58.00   Length: 30
Percent Similarity: 100.00%   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 5   Mismatches: 0
  Indels: 0
  Gaps: 0

US-09-976-740-22 (1-10) x AAH26505 (1-30)

```
Qy  1 GluAspAlaSpProAspGlyPheLeuGly 10
        |||||||||||||||||||||||||||||
Db  1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30
```

RESULT 2
ID AAC59574/c
AC AAC59574;
DT 26-JAN-2001 (first entry)
DE Human secreted protein gene 9 SEQ ID NO:19,
KW Human; secreted protein; diagnosis; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active general; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW and antibacterial; gene therapy; detection; cancer; chromosome marker;
KW chromosome identification; neural disorder; immune disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; wound healing; infectious disease; preservative;
KW food additive; ss.
CS Homo sapiens.
XX
PN WO200056683-A1.
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US006822.
XX
PR 23-MAR-1999; 99US-0126054P.
PR 10-DEC-1999; 99US-0169916P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-587666/55.
DR P-PSDB; AAB34307.
XX
PT Human secreted proteins and gene sequences encoding them, useful for
PT detecting, preventing, and treating disorders such as cancer,
PT neurological disorders and immune system disorders.
XX

PS
Claim 1; Page 344; 429pp; English.
XX
CC The polynucleotide sequences given in AAC59566 to AAC59614 encode the
CC human secreted proteins given in AAB34299 to AAB34347. AAB34348 to
CC AAB34437 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular
CC active general; vulnerary; gastrointestinal; nephrotropic; antiinfective;
CC gynaecological; and antibacterial. The polynucleotides can be used for
CC the detection of various disorders such as cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The secreted proteins can be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wound healing, and infectious diseases. The proteins can also
CC be used as a food additive or preservative to increase or decrease
CC storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 0.133
Score: 58.00   Length: 1134
Percent Similarity: 100.00%   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 3   Mismatches: 0
  Indels: 0
  Gaps: 0

US-09-976-740-22 (1-10) x AAC59574 (1-1134)

```
Qy   1 GluAspAlaSpProAspGlyPheLeuGly 10
         |||||||||||||||||||||||||||||
Db 495 GAGGATGATGACCCCGATGGCTTCTTAGGC 466
```

RESULT 3
ID AAV32838
AC AAV32838;
DT 09-NOV-1998 (first entry)
DE Human low density lipoprotein binding protein LBP-2 cDNA.
KW Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.
CS Homo sapiens.
XX

FH Key	Location/Qualifiers
FT CDS	1..654
FT	/tag= a
FT misc_feature	22..99
FT	/tag= c
FT	/note= "Claim 13"
FT misc_feature	22..66
FT	/tag= b
FT	/note= "Claim 12"
FT misc_feature	67..99
FT	/tag= d
FT	/note= "Claim 14"
FT misc_feature	622..651
FT	/tag= e
FT	/note= "Claim 15"

XX
PN WO9823282-A1.
PD 04-JUN-1998.
XX
PF 26-NOV-1997; 97WO-US021857.

XX
PR   27-NOV-1996;   96US-0031930P.
PR   03-JUN-1997;   97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49041.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 9; Fig 16; 47pp; English.
XX
CC   This cDNA clone codes for novel human low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49041). It was isolated by screening human
CC   liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA
CC   clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
CC   42) are claimed. An abnormality in LBP metabolism or structure is
CC   diagnostic of a risk for atherosclerosis. The invention provides: methods
CC   for determining if an animal is at risk for atherosclerosis (e.g. for
CC   prenatal screening); methods for treating atherosclerosis (including gene
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP.
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
         ||||||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AAV32838 (1-1208)

Alignment Scores:
Pred. No.:
Score: 0.143   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 2   Indels: 0
                                      Gaps: 0

RESULT 4
AAH26494
ID   AAH26494 standard; cDNA; 1208 BP.
XX
AC   AAH26494;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerosis; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..654
FT   /*tag= a
FT   /partial
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX

PF   28-FEB-2001;   2001WO-US006356.
XX
PR   02-MAR-2000;   2000US-00517849.
PR   14-JUL-2000;   2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82803.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
Example 4; Fig 16; 143pp; English.
XX
CC   The present sequence is that of a partial cDNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC   isolated from human foetal brain, liver and aorta cDNA libraries using
CC   rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC   AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides capable of binding to native and methylated LDL. Also
CC   claimed are isolated LBP polypeptides, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, and methods for evaluating an agent for use in treating
CC   atherosclerosis, methods for treating a cell having an abnormality in
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
         ||||||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

US-09-976-740-22 (1-10) x AAH26494 (1-1208)

Alignment Scores:
Pred. No.:
Score: 0.143   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 5   Indels: 0
                                      Gaps: 0

RESULT 5
AAF21860
ID   AAF21860 standard; DNA; 1336 BP.
XX
AC   AAF21860;
XX
DT   27-MAR-2001 (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 247.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO20005173-A1.
XX
PD   21-SEP-2000.
XX

```
RESULT 6
AAH26499

ID   AAH26499 standard; DNA; 1614 BP.
XX
AC   AAH26499;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200164874-A2.
XX
PD   08-MAR-2000; 2000WO-US005881.
XX
PF
PR   12-MAR-1999;  99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58957.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention, treatment
PT   and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT   neurological diseases.
XX
PS   Claim 1; Page 670-671; 1299pp; English.
XX
CC   Sequences AAP21614 - AAP22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAP22032 - AAP22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemia; wound healing;
CC   neurological diseases such as cerebral anoxia and epilepsy; and
CC   infectious diseases
XX
SQ   Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;
XX

Alignment Scores:
Pred. No.:
Score:                   0.159
Percent Similarity:     58.00        Length:         1336
Best Local Similarity: 100.00%       Matches:        10
Query Match:           100.00%       Conservative:   0
                                     Mismatches:     0
                          3          Indels:         0
DB:                                  Gaps:           0

US-09-976-740-22 (1-10) x AAF21860 (1-1336)

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db  694 GAGGATGATGACCCGATGGCTTCTTAGGC 723
```

```
RESULT 7
AAH26495

ID   AAH26495 standard; DNA; 12425 BP.
XX
AC   AAH26495;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) gene.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2832..5153
FT                   /*tag= a
FT                   /note= "includes introns"
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-5655505/63.
DR   P-PSDB; AAB82806.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Claim 7; Fig 7A; 143pp; English.
XX
CC   The present sequence is that of the coding region of the human gene (see
CC   also AAH26494) encoding novel human low density lipoprotein binding
CC   protein 2 (LBP-2; see AAB82806). The gene was isolated from a genomic DNA
CC   library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the
CC   present sequence differs from that predicted from a cDNA clone (see
CC   AAB82803) in that it contains an additional 321 amino acids at its N-
CC   terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among
CC   claimed polynucleotides of the invention that encode novel polypeptides
CC   capable of binding to native and methylated LDL. Also claimed are
CC   isolated LBP polypeptides, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, methods and methods for evaluating an agent for use in
CC   treating atherosclerosis, and methods for treating a cell having an abnormality in
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.:
Score:                   0.196
Percent Similarity:     58.00        Length:         1614
Best Local Similarity: 100.00%       Matches:        10
Query Match:           100.00%       Conservative:   0
DB:                       5          Mismatches:     0
                                     Indels:         0
                                     Gaps:           0

US-09-976-740-22 (1-10) x AAH26495 (1-1614)

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db 1585 GAGGATGATGACCCGATGGCTTCTTAGGC 1614
```

Left column:

```
FT   exon        2832..3785
FT   intron      3786..4207      /*tag= b
FT                               /*tag= 4207
FT   exon        4208..4502      /*tag= c
FT   intron      4503..4593      /*tag= d
FT   intron      4503..4593      /*tag= e
FT   exon        4594..4694      /*tag= e
FT   exon        4594..4694      /*tag= f
FT   intron      4695..4787      /*tag= f
FT   exon        4788..4899      /*tag= g
FT   exon        4788..4899      /*tag= g
FT   intron      4900..4994      /*tag= h
FT   intron      4900..4994      /*tag= i
FT   exon        4995..5153      /*tag= i
FT   exon        4995..5153      /*tag= j
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 4; Fig 23; 143pp; English.
XX
CC   The present sequence is that of genomic DNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was
CC   isolated from a human genomic library by screening with LBP-2 cDNA (see
CC   AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides, termed LBPs, capable of binding to native and
CC   methylated LDL. Also claimed are isolated LBP polypeptides, and
CC   biologically active fragments and analogues of them, as well as
CC   expression vectors, cells and methods of producing the LBPs. Methods of
CC   determining if an animal is at risk for atherosclerosis, methods for
CC   evaluating an agent for use in treating atherosclerosis, and methods for
CC   treating a cell having an abnormality in structure or metabolism of LBP
CC   are claimed. Pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions, are also claimed
XX
SQ   Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;
```

US-09-976-740-22 (1-10) x AAH26495 (1-12425)

Alignment Scores:
```
Pred. No.:              1.82
Score:                  58.00                Length:          12425
Percent Similarity:     100.00%    Matches:            10
Best Local Similarity:  100.00%    Conservative:        0
Query Match:            5           Mismatches:         0
DB:                                 Indels:             0
                                    Gaps:               0
```

RESULT 8
AAH26495
```
Db   5121 GAGGATGATGACCCGATGGCTTCTTAGGC 5150

Qy      1 GluAspAspProAspGlyPheLeuGly 10
          ||||||||||||||||||||||||||||
```

Right column:

```
ID   AAH26489 standard; cDNA; 1362 BP.
XX
AC   AAH26489;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FH   CDS             1..955
FT                   /*tag= a
FT                   /partial
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 12; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82799) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at risk for atherosclerosis, methods for evaluating an agent for use
CC   in treating atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;
```

US-09-976-740-22 (1-10) x AAH26489 (1-1362)

Alignment Scores:
```
Pred. No.:              0.941
Score:                  54.00                Length:          1362
Percent Similarity:     100.00%    Matches:             9
Best Local Similarity:  90.00%     Conservative:        1
Query Match:            5           Mismatches:         0
DB:                                 Indels:             0
                                    Gaps:               0
```

RESULT 9
AAH26489
```
Db   667 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696

Qy      1 GluAspAspAspProAspGlyPheLeuGly 10
          ||||||||||:::||||:||||||||||
```

Left column

```
ID   AAH26490 standard; cDNA; 1422 BP.
XX
AC   AAH26490;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.
XX
KW   Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..955
FT                   /*tag= a
FT                   /partial
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82800.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 13; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82800) of
CC   novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in
CC   AAZ26491. The invention provides claimed polynucleotides encoding novel
CC   polypeptides which are capable of binding to native and methylated LDL,
CC   the isolated polypeptides, termed LBPs, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Also claimed are methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1422 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:			
Score:	0.986	Length:	1422
Percent Similarity:	54.00	Matches:	1422
Best Local Similarity:	100.00%	Mismatches:	9
Query Match:	90.00%	Conservative:	1
	93.10%	Indels:	0
DB:	5	Gaps:	0

```
US-09-976-740-22 (1-10) x AAH26490 (1-1422)

Qy      1 GluAspAspProAspGlyPheLeuGly 10
            |||||||||||||::||||||:||||||
Db    727 GAGGACGATGACCCCGGAAGGCTTCTCTGGGA 756
```

Right column

```
RESULT 10
ID   AAV32835 standard; cDNA; 1617 BP.
XX
AC   AAV32835;
XX
DT   09-NOV-1998 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW   receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..954
FT                   /*tag= a
XX
FT   misc_feature    156..1617
FT                   /*tag= b
FT   misc_feature    156..954
FT                   /note= "Claim 5"
FT   misc_feature    196..1617
FT                   /*tag= c
FT                   /note= "Claim 6"
FT   misc_feature    313..396
FT                   /note= "Claim 5"
FT   misc_feature    313..360
FT                   /*tag= f
FT                   /note= "Claim 19"
FT   misc_feature    313..360
FT                   /*tag= e
FT                   /note= "Claim 18"
FT   misc_feature    361..396
FT                   /*tag= g
FT                   /note= "Claim 20"
FT   misc_feature    631..660
FT                   /*tag= h
FT                   /note= "Claim 21"
XX
PN   WO9823282-A1.
XX
PD   04-JUN-1998.
XX
PF   26-NOV-1997; 97WO-US021857.
XX
PR   27-NOV-1996; 96US-0031930P.
PR   03-JUN-1997; 97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-3224455/28.
DR   P-PSDB; AAW49038.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 4; Fig 11; 47pp; English.
XX
CC   This cDNA clone codes for novel rabbit low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49038). It was isolated by functional
CC   screening of a cDNA library, produced from balloon-deendothelialised
CC   healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to
CC   bind both native and methyl LDL. cDNA clones (see AAV32834-39) and
CC   encoded rabbit and human LBPs (see AAW49037-42) are claimed. An
CC   abnormality in an aspect of LBP metabolism or structure is diagnostic of
CC   a risk for atherosclerosis. The invention provides: methods for
CC   determining if an animal is at risk for atherosclerosis (e.g. for
CC   prenatal screening); methods for treating atherosclerosis (including gene
```

Left column

```
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP
XX
SQ   Sequence 1617 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.14
Score:                  54.00
Percent Similarity:     100.00%
Best Local Similarity:  90.00%
Query Match:            93.10%
DB:

                        Length:         1617
                        Matches:        9
                        Conservative:   1
                        Mismatches:     0
                        Indels:         0
                        Gaps:           0

US-09-976-740-22 (1-10) x AAV32835 (1-1617)

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        |||||||||||||||||:::||||||||||||
Db  922 GAGGACGATGACCCGGACGGGAAGGCTTCCTGGGA 951
```

```
RESULT 11
AAH26488
ID   AAH26488 standard; cDNA; 1617 BP.
XX
AC   AAH26488;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..955
FT                  /*tag= a
FT                  /partial
FT                  /note="includes in-frame stop codon at nucleotides
FT                  28..30"
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051789.
PR   14-JUL-2000; 2000US-0061289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82798.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 11; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82798) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
```

Right column

```
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at-risk for atherosclerosis, and methods for evaluating an agent for use
CC   in treating atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1617 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.14
Score:                  54.00
Percent Similarity:     100.00%
Best Local Similarity:  90.00%
Query Match:            93.10%
DB:

                        Length:         1617
                        Matches:        9
                        Conservative:   1
                        Mismatches:     0
                        Indels:         0
                        Gaps:           0

US-09-976-740-22 (1-10) x AAH26488 (1-1617)

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        |||||||||||||||||:::||||||||||||
Db  922 GAGGACGATGACCCGGACGGGAAGGCTTCCTGGGA 951
```

```
RESULT 12
AAH26500
ID   AAH26500 standard; cDNA; 2561 BP.
XX
AC   AAH26500;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key            Location/Qualifiers
FT   CDS            246..1928
FT                  /*tag= a
XX
PN   WO20016874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051789.
PR   14-JUL-2000; 2000US-0061289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82807.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Claim 4; Fig 2A; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding novel rabbit low density
CC   lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was
CC   isolated following screening of a rabbit cDNA library for clones encoding
CC   LBPs that bound to both native low density lipoprotein (LDL) and methyl
CC   LDL. The invention provides claimed polynucleotides encoding novel
CC   polypeptides which are capable of binding to native and methylated LDL,
CC   the isolated polypeptides, termed LBPs, and biologically active fragments
```

```
CC  and analogues of them, as well as expression vectors, cells and methods
CC  of producing the LBPs. Also claimed are methods of determining if an
CC  animal is at risk for atherosclerosis, methods for evaluating an agent
CC  for use in treating atherosclerosis, and methods for treating a cell
CC  having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC  compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC  compositions, are also claimed
XX
SQ  Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.88
Score:                  54.00
Percent Similarity:     100.00%       Length:        2561
Best Local Similarity:  90.00%        Matches:       9
Query Match:            93.10%        Conservative:  1
DB:                     5             Mismatches:    0
                                      Indels:        0
                                      Gaps:          0

US-09-976-740-22 (1-10) x AAH26500 (1-2561)

Qy      1 GluAspAspAspProAspGlyPheLeuGly 10
          ||||||||||||||||||||||||||||||||
Db   1866 GAGGAGGAGATGACCCCGGAAGGCTTCCTGGGA 1895


RESULT 13
ID  ABX57356 standard; DNA; 539 BP.
AC  ABX57356;
XX
DT  20-FEB-2003 (first entry)
XX
DE  Arabidopsis thaliana polynucleotide #708.
XX
KW  Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
KW  genetic modification; environmental stress; disease resistance;
KW  fungicide; insecticide; stress tolerance.
XX
OS  Arabidopsis thaliana.
XX
PN  US200204089-A1.
XX
PD  04-APR-2002.
XX
PF  26-JAN-2001; 2001US-00770152.
XX
PR  27-JAN-2000; 2000US-0178503P.
XX
PA  (GORL/) GORLACH J.
PA  (ANYY/) AN Y.
PA  (HAMI/) HAMILTON C M.
PA  (PRIC/) PRICE J L.
PA  (RAIN/) RAINES T M.
PA  (YUYY/) YU Y.
PA  (RAME/) RAMEAKA J G.
PA  (PAGE/) PAGE A.
PA  (MATH/) MATHEW A V.
PA  (LEDF/) LEDFORD B L.
PA  (WOES/) WOESSNER J P.
PA  (HAAS/) HAAS W D.
PA  (GARC/) GARCIA C A.
PA  (KRIC/) KRICKER M.
PA  (SLAT/) SLATER T.
PA  (DAVI/) DAVIS K R.
PA  (ALLE/) ALLEN K.
PA  (HOFF/) HOFFMAN N.
PA  (HURB/) HURBAN P.
XX

Gorlach J,  An Y,  Hamilton CM,  Price JL,  Raines TM,  Yu Y;  Haas WD;
Rameaka JG,  Page A,  Mathew AV,  Ledford BL,  Woessner JP,  Haas WD;
Garcia CA,  Kricker M,  Slater T,  Davis KR,  Allen K,  Hoffman N;
Hurban P;
```

```
DR  WPI; 2003-110410/10.
XX
PT  Novel Arabidopsis thaliana nucleic acid useful for identifying homologous
PT  or related genes, and to create genetically modified and transgenic
PT  organisms, such as plant cells and plants.
XX
PS  Claim 1; SEQ ID NO 708; 45pp; English.
XX
CC  The invention relates to Arabidopsis thaliana nucleic acid sequences. The
CC  DNA sequences and the polypeptides they encode are useful for identifying
CC  homologous or related genes, for producing compositions that modulate the
CC  expression or function of the polypeptides, for mapping functional
CC  regions of the protein, in diagnosis, for studying associated
CC  physiological pathways, for genetic manipulation of cells, preferably
CC  plant cells, in screening assays of various plant strains to determine
CC  the strains that are capable of withstanding a particular disease or
CC  environmental stress, for enhancing or inhibiting production of
CC  biosynthetic products in plants and to create genetically modified and
CC  transgenic organisms, such as plant cells and plants. Transgenic plants
CC  are useful for introducing or improving disease resistance and stress
CC  tolerance in plants, screening biologically active agents, such as
CC  fungicides and insecticides, and for elucidating biochemical pathways.
CC  Sequences ABX56649-ABX57647 represent Arabidopsis thaliana
CC  polynucleotides of the invention. Note: The sequence data for this patent
CC  did not form part of the printed specification but was obtained in
CC  electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ  Sequence 539 BP; 130 A; 151 C; 100 G; 158 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              27.5
Score:                  44.00
Percent Similarity:     80.00%        Length:        539
Best Local Similarity:  80.00%        Matches:       8
Query Match:            75.86%        Conservative:  0
DB:                     7             Mismatches:    2
                                      Indels:        0
                                      Gaps:          0

US-09-976-740-22 (1-10) x ABX57356 (1-539)

Qy      1 GluAspAspAspProAspGlyPheLeuGly 10
          ||||||    ||||||||||||||||||||
Db    355 GAGGAATCGTGATCCTCAAGGCTTCCTTGGA 384


RESULT 14
ID  ABZ14501 standard; DNA; 2838 BP.
AC  ABZ14501;
XX
DT  21-JAN-2003 (first entry)
XX
DE  Arabidopsis thaliana stress regulated gene SEQ ID NO 2306.
XX
KW  Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS  Arabidopsis thaliana.
XX
PN  WO200216655-A2.
XX
PD  28-FEB-2002.
XX
PF  24-AUG-2001; 2001WO-US026685.
XX
PR  24-AUG-2000; 2000US-02278866P.
PR  26-JAN-2001; 2001US-0264647P.
PR  22-JUN-2001; 2001US-0300101P.
XX
PA  (SCRI ) SCRIPPS RES INST.
PA  (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI  Harper JF,  Kreps J,  Wang X,  Zhu T;
XX
DR  WPI; 2002-304127/34.
```

XX
PT   Identifying a stress condition to which a plant cell has been exposed and
PT   producing plants with increased tolerance to these abiotic stresses.
XX
PS   Claim 144; SEQ ID NO 2306; 577pp + Sequence Listing; English.
XX
CC   The invention relates to identifying a stress condition to which a plant
CC   cell has been exposed, comprising: (a) contacting nucleic acid
CC   representative of expressed polynucleotides in the plant cell with an
CC   array or probes representative of the plant cell genome; and (b)
CC   detecting a profile of expressed polynucleotides in the plant cell
CC   characteristic of a stress response. The method is useful in the
CC   production of transgenic plants, cells and seeds and in producing plants
CC   with increased tolerance to abiotic stress. The present sequence is that
CC   of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC   in methods of the invention. Note: The sequence data for this patent is
CC   not represented in the printed specification but is based on sequence
CC   information supplied to Derwent by the European Patent Office
XX
SQ   Sequence 2838 BP; 784 A; 600 C; 703 G; 751 T; 0 U; 0 Other;

US-09-976-740-22 (1-10) x ABZ14501 (1-2838)

Alignment Scores:
Pred. No.:
Score: 169   Length: 2838
Percent Similarity: 44.00   Matches: 8
Best Local Similarity: 80.00%   Conservative: 0
Query Match: 80.00%   Mismatches: 2
DB: 75.86%   Indels: 0
                             6   Gaps: 0

Qy   1 GluAspAspProAspGlyPheLeuGly 10
        ||||| ||||||||
Db 352 GAGGATCGTGATCCTCAAGGCTTCCTTGGA 381

CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 2838 BP; 784 A; 600 C; 703 G; 751 T; 0 U; 0 Other;

US-09-976-740-22 (1-10) x ADA68111 (1-2838)

Alignment Scores:
Pred. No.:
Score: 169   Length: 2838
Percent Similarity: 44.00   Matches: 8
Best Local Similarity: 80.00%   Conservative: 0
Query Match: 80.00%   Mismatches: 2
DB: 75.86%   Indels: 0
                             7   Gaps: 0

Qy   1 GluAspAspProAspGlyPheLeuGly 10
        ||||| ||||||||
Db 352 GAGGATCGTGATCCTCAAGGCTTCCTTGGA 381

Search completed: March 12, 2004, 21:08:47
Job time : 21.8507 secs

RESULT 15
ADA68111
ID   ADA68111 standard; DNA; 2838 BP.
XX
AC   ADA68111;
XX
DT   20-NOV-2003 (first entry)
XX
DE   Arabidopsis thaliana gene, SEQ ID 374.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200300898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI   Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 6; SEQ ID NO 374; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 20:05:17 ; Search time 3.39045 Seconds
(without alignments)
1636.805 Million cell updates/sec

Title: US-09-976-740-22
Perfect score: 58
Sequence: 1 EDDDPDGFLG 10

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19564/app_query.fasta_1.1898
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human a0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0997674 0 @CGN_1_1_235 @runat_10032004_094549_19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	30	4	US-08-979-608A-33	Sequence 33, Appl
2	58	100.0	30	4	US-09-517-849-33	Sequence 33, Appl
3	58	100.0	30	4	US-09-616-289-33	Sequence 33, Appl
4	58	100.0	425	4	US-09-621-976-9791	Sequence 9791, Ap
5	58	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appl
6	58	100.0	1208	4	US-09-517-849-16	Sequence 16, Appl
7	58	100.0	1208	4	US-09-616-289-16	Sequence 16, Appl
8	58	100.0	1614	4	US-09-616-289-45	Sequence 45, Appl
9	58	100.0	12425	4	US-09-616-289-50	Sequence 50, Appl
10	54	93.1	1362	4	US-08-979-608A-12	Sequence 12, Appl
11	54	93.1	1362	4	US-09-517-849-12	Sequence 12, Appl
12	54	93.1	1362	4	US-09-616-289-12	Sequence 12, Appl
13	54	93.1	1422	4	US-08-979-608A-13	Sequence 13, Appl
14	54	93.1	1422	4	US-09-517-849-13	Sequence 13, Appl
15	54	93.1	1422	4	US-09-616-289-13	Sequence 13, Appl
16	54	93.1	1617	4	US-08-979-608A-11	Sequence 11, Appl
17	54	93.1	1617	4	US-09-517-849-11	Sequence 11, Appl
18	54	93.1	2561	4	US-09-616-289-11	Sequence 11, Appl
19	54	93.1	2561	4	US-09-616-289-48	Sequence 48, Appl
20	54	70.7	486	4	US-09-621-976-3195	Sequence 3195, App
21	54	70.7	2043	4	US-09-614-912-1171	Sequence 1171, App
22	54	69.0	1656	4	US-09-252-991A-8924	Sequence 8924, Ap
23	54	67.2	111282	4	US-09-754-250-3	Sequence 3, Appli
24	38	65.5	5410	4	US-09-221-017B-70	Sequence 70, Appl
25	37	63.8	642	4	US-08-956-171E-614	Sequence 614, Appl
26	37	63.8	648	4	US-09-228-986-26	Sequence 26, Appl
27	37	63.8	699	4	US-09-252-991A-575	Sequence 575, Appl
28	37	63.8	900	4	US-09-589-927-7	Sequence 7, Appli
29	37	63.8	900	4	US-09-277-665-7	Sequence 7, Appli
30	37	63.8	900	4	US-09-589-987-7	Sequence 7, Appl
31	37	63.8	1269	4	US-09-489-039A-979	Sequence 979, Appl
32	37	63.8	1368	2	US-08-738-172-3	Sequence 3, Appli
33	37	63.8	1416	4	US-09-711-164-273	Sequence 273, App
34	37	63.8	1425	4	US-09-489-039A-1173	Sequence 1173, App
35	37	63.8	1434	4	US-09-489-039A-522	Sequence 522, App
36	37	63.8	1458	4	US-09-252-991A-599	Sequence 599, App
37	37	63.8	2936	2	US-08-738-172-1	Sequence 1, Appli
38	37	63.8	4454	2	US-08-738-172-2	Sequence 2, Appli
39	36	63.8	284	4	US-09-016-434-416	Sequence 416, Appli
40	36	62.1	297	4	US-09-252-991A-8030	Sequence 8030, Ap
41	36	62.1	357	4	US-09-894-844-102	Sequence 102, App
42	36	62.1	477	4	US-09-446-754-7	Sequence 7, Appli
43	36	62.1	507	4	US-09-252-991A-14417	Sequence 14417, A
44	36	62.1	606	4	US-09-252-991A-3463	Sequence 3463, Ap
45	36	62.1	891	4	US-09-252-991A-8283	Sequence 8283, Ap

ALIGNMENTS

RESULT 1
US-08-979-608A-33
Sequence 33, Application US/08979608A
Patent No. 6355451.

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6355451-1997
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 30 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..30
  SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-08-979-608A-33

Alignment Scores:
Pred. No.:
Score: 0.000437   Length: 30
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

US-08-979-608A-33

Qy 1 GluAspAspAspProAspGlyPheLeuGly 10
      ||||||||||||||||||||||||||||||
Db 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x US-08-979-608A-33 (1-30)

RESULT 2
US-09-517-849-33
Sequence 33, Application US/0951784 9
Patent No. 6605588
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
             Lees, Robert S.
             Law, Simon W.
             Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
    BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
    TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
  STREET: 225 Franklin Street
  CITY: Boston
  STATE: MA
  COUNTRY: USA
  ZIP: 02110-2804
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/517,849
  FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/979,608
  FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Myers, Louis
  REGISTRATION NUMBER: 35,965
  REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617/542-5070
  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 30 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single

  TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..30
  SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-517-849-33

Alignment Scores:
Pred. No.:
Score: 0.000437   Length: 30
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

US-09-976-740-22 (1-10) x US-09-517-849-33 (1-30)

Qy 1 GluAspAspAspProAspGlyPheLeuGly 10
      ||||||||||||||||||||||||||||||
Db 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

RESULT 3
US-09-616-289-33
Sequence 33, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
  APPLICANT: Lees, Robert S.
  APPLICANT: Law, Simon W.
  APPLICANT: Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
  TITLE OF INVENTION: ATHEROSCLEROSIS
  FILE REFERENCE: 10797-004001
  CURRENT APPLICATION NUMBER: US/09/616,289
  CURRENT FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: US 09/517,849
  PRIOR FILING DATE: 2000-03-02
  PRIOR APPLICATION NUMBER: US 08/979,608
  PRIOR FILING DATE: 1997-11-26
  PRIOR APPLICATION NUMBER: US 60/031,930
  PRIOR FILING DATE: 1996-11-27
  PRIOR APPLICATION NUMBER: US 60/048,547
  PRIOR FILING DATE: 1997-06-03
  NUMBER OF SEQUENCES: 53
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 33
  LENGTH: 30
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-616-289-33

  TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..30
  SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-616-289-33

Alignment Scores:
Pred. No.:
Score: 0.000437   Length: 30
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

Qy 1 GluAspAspAspProAspGlyPheLeuGly 10
      ||||||||||||||||||||||||||||||
Db 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x US-09-616-289-33 (1-30)

RESULT 4
US-09-621-976-9791
Sequence 9791, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
  APPLICANT: Dumas Milne Edwards, J.B.
  APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054P2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm

SEQ ID NO 9791
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9791

Alignment Scores:
Pred. No.:
Score: 0.00805   Length: 425
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                             Gaps: 0

US-09-976-740-22 (1-10) x US-09-621-976-9791 (1-425)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
          |||||||||||||||||||||||||||
Db   200 GAGGATGATGACCCCGATGGCTTCTTAGGC 229

RESULT 5
US-08-979-608A-16
; Sequence 16, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   ZIP: 02110-2804
;   COUNTRY: USA
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/979,608A
;   FILING DATE: 26-No. 6355451-1997
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/048,547
;   FILING DATE: 03-JUN-1997
;   APPLICATION NUMBER: US 60/031,930
;   FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

; FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..651
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16

Alignment Scores:
Pred. No.:
Score: 0.0254   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                             Gaps: 0

US-09-976-740-22 (1-10) x US-08-979-608A-16 (1-1208)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
          |||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 6
US-09-517-849-16
; Sequence 16, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   ZIP: 02110-2804
;   COUNTRY: USA
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/517,849
;   FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/979,608
;   FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..651
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-517-849-16

Alignment Scores:
Pred. No.:
Score: 0.0254   Length: 1208
                                             Matches: 10

```
Percent Similarity:       100.00%     Conservative:  0
Best Local Similarity:    100.00%     Mismatches:    0
Query Match:              100.00%     Indels:        0
DB:                       4           Gaps:          0

US-09-976-740-22 (1-10) x US-09-517-849-16 (1-1208)

Qy        1 GluAspAspProAspGlyPheLeuGly 10
            ||||||||||||||||||||||||||||
Db      622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

RESULT 7
US-09-616-289-16
; Sequence 16, Application US/0961629
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-616-289-16

Alignment Scores:
```
Pred. No.:                0.0254
Score:                    58.00
Percent Similarity:       100.00%     Length:        1208
Best Local Similarity:    100.00%     Matches:       10
Query Match:              100.00%     Conservative:  0
DB:                       4           Mismatches:    0
                                      Indels:        0
                                      Gaps:          0
```

US-09-976-740-22 (1-10) x US-09-616-289-16 (1-1208)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
            ||||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

RESULT 8
US-09-616-289-45
; Sequence 45, Application US/0961629
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-616-289-45

Alignment Scores:
```
Pred. No.:                0.0349
Score:                    58.00
Percent Similarity:       100.00%     Length:        1614
Best Local Similarity:    100.00%     Matches:       10
Query Match:              100.00%     Conservative:  0
DB:                       4           Mismatches:    0
                                      Indels:        0
                                      Gaps:          0
```

US-09-976-740-22 (1-10) x US-09-616-289-45 (1-1614)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
            ||||||||||||||||||||||||||||
Db   1585 GAGGATGATGACCCCGATGGCTTCTTAGGC 1614
```

RESULT 9
US-09-616-289-50
; Sequence 50, Application US/0961629
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-50

Alignment Scores:
```
Pred. No.:   0.33
Score: 58.00
Percent Similarity: 100.00%   Length: 12425
Best Local Similarity: 100.00%   Matches: 10
Query Match: 100.00%   Conservative: 0
DB: 4   Mismatches: 0
                                      Indels: 0
                                      Gaps: 0
```

US-09-976-740-22 (1-10) x US-09-616-289-50 (1-12425)

```
Qy    1 GluAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db 5121 GAGGATGATGACCCCGATGGCTTCTTAGGC 5150
```

RESULT 10
US-08-979-608A-12
; Sequence 12, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-No. 6355451-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..696
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-979-608A-12

Alignment Scores:
Pred. No.:
Score: 0.17   Length: 1362
Percent Similarity: 54.00   Matches: 9
Best Local Similarity: 100.00%   Conservative: 1
Query Match: 90.00%   Mismatches: 0
DB: 93.10%   Indels: 0
                       4   Gaps: 0

US-09-976-740-22 (1-10) x US-08-979-608A-12 (1-1362)

```
Qy   1 GluAspAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||
Db 667 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696
```

RESULT 11

US-09-517-849-12
; Sequence 12, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,849
; FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..696
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-517-849-12

Alignment Scores:
Pred. No.:
Score: 0.17   Length: 1362
Percent Similarity: 54.00   Matches: 9
Best Local Similarity: 100.00%   Conservative: 1
Query Match: 90.00%   Mismatches: 0
DB: 93.10%   Indels: 0
                       4   Gaps: 0

US-09-976-740-22 (1-10) x US-09-517-849-12 (1-1362)

```
Qy   1 GluAspAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||
Db 667 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696
```

RESULT 12
US-09-616-289-12
; Sequence 12, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 12
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(696)
US-09-616-289-12

Alignment Scores:
Pred. No.:   Length: 1362
Score: 0.17   Matches: 9
Percent Similarity: 54.00   Conservative: 1
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 90.00%   Indels: 0
DB: 93.10%   Gaps: 0
                          4

US-09-976-740-22 (1-10) x US-09-616-289-12 (1-1362)

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||:|:|||||||||||
Db 667 GAGGACGATGACCCCGAAGGCTTCCTGGGA 696

RESULT 13
US-08-979-608A-13
; Sequence 13, Application US/0897960A
; Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
           Lees, Robert S.
           Law, Simon W.
           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                    BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                    TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO- 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...756
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-979-608A-13

Alignment Scores:
Pred. No.:   Length: 1422
Score: 0.178   Matches: 9
Percent Similarity: 54.00   Conservative: 1
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 90.00%   Indels: 0
DB: 93.10%   Gaps: 0
                          4

US-09-976-740-22 (1-10) x US-08-979-608A-13 (1-1422)

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||:|:|||||||||||
Db 727 GAGGACGATGACCCCGAAGGCTTCCTGGGA 756

RESULT 14
US-09-517-849-13
; Sequence 13, Application US/0951789A
; Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
           Lees, Robert S.
           Law, Simon W.
           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                    BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                    TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
TYPE: nucleic acid

```
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       FEATURE:
;           NAME/KEY:   Coding Sequence
;           LOCATION:   1...756
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-517-849-13

Alignment Scores:
Pred. No.:              0.178           Length:         1422
Score:                  54.00           Matches:        9
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.00%          Mismatches:     0
Query Match:            93.10%          Indels:         0
DB:                     4               Gaps:           0

US-09-976-740-22  (1-10)  x  US-09-517-849-13  (1-1422)

Qy           1 GluAspAAspAspProAspGlyPheLeuGly 10
               |||||||||||||||||||||::|||||||||||
Db         727 GAGGACCATGACCCGGAAGGCTTCCTGGGA 756

RESULT 15
US-09-616-289-13
; Sequence 13, Application US/0916289
; Patent No. 6632923
; GENERAL INFORMATION:
;   APPLICANT:  Lees, Ann M.
;   APPLICANT:  Lees, Robert S.
;   APPLICANT:  Law, Simon W.
;   APPLICANT:  Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;   TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;   TITLE OF INVENTION: ATHEROSCLEROSIS
;   FILE REFERENCE: 10797-004001
;   CURRENT APPLICATION NUMBER: US/09/616,289
;   CURRENT FILING DATE:  2000-07-14
;   PRIOR APPLICATION NUMBER: US 09/517,849
;   PRIOR FILING DATE: 2000-03-02
;   PRIOR APPLICATION NUMBER: US 08/979,608
;   PRIOR FILING DATE: 1997-11-26
;   PRIOR APPLICATION NUMBER: US 60/031,930
;   PRIOR FILING DATE: 1996-11-27
;   PRIOR APPLICATION NUMBER: US 60/048,547
;   PRIOR FILING DATE: 1997-06-03
;   NUMBER OF SEQ ID NOS: 53
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 13
;       LENGTH: 1422
;       TYPE: DNA
;       ORGANISM: Oryctolagus cuniculus
;       FEATURE:
;           NAME/KEY:   CDS
;           LOCATION:   (1)...(756)
US-09-616-289-13

Alignment Scores:
Pred. No.:              0.178           Length:         1422
Score:                  54.00           Matches:        9
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  90.00%          Mismatches:     0
Query Match:            93.10%          Indels:         0
DB:                     4               Gaps:           0

US-09-976-740-22  (1-10)  x  US-09-616-289-13  (1-1422)

Qy           1 GluAspAspAspProAspGlyPheLeuGly 10
               |||||||||||||||||::|||||||||||||
Db         727 GAGGACGATGACCCGGAAGGCTTCCTGGGA 756
```

Search completed: March 13, 2004, 04:06:29
Job time : 6 39045 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 20:46:42 ; Search time 14.4676 Seconds
(without alignments)
2544.725 Million cell updates/sec

Title: US-09-976-740-22
Perfect score: 58
Sequence: 1 EDDDPDGFLG 10

Scoring table: BLOSUM62
         Xgapop 10.0 , Xgapext 0.5
         Ygapop 10.0 , Ygapext 0.5
         Fgapop 6.0 , Fgapext 7.0
         Delop   6.0 , Delext 7.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4665114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19588/app_query.fasta_1.1898
-Db=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NOM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09976740 @CGN 1 1.712 @runat 10032004 094549 19588
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US1A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	%	Query Match Length	DB ID	Description
1	58	100.0	30	9	US-09-962-055-33	Sequence 33, App1
2	58	100.0	30	9	US-09-976-740-16	Sequence 16, App1
3	58	100.0	30	12	US-10-671-242-33	Sequence 33, App1
4	58	100.0	30	12	US-10-023-529-33	Sequence 33, App1
5	58	100.0	30	13	US-10-023-523-33	Sequence 33, App1
6	58	100.0	30	15	US-10-616-187-16	Sequence 16, App1
7	58	100.0	30	15	US-10-616-187-33	Sequence 33, App1
8	58	100.0	30	9	US-09-962-055-16	Sequence 16, App1
9	58	100.0	1208	12	US-09-976-740-16	Sequence 16, App1
10	58	100.0	1208	12	US-10-671-242-16	Sequence 16, App1
11	58	100.0	1208	13	US-10-023-529-16	Sequence 16, App1
12	58	100.0	1208	12	US-10-023-523-16	Sequence 16, App1
13	58	100.0	1336	14	US-10-616-187-16	Sequence 16, App1
14	58	100.0	1445	10	US-09-945-527-6	Sequence 6, App1
15	58	100.0	1614	9	US-09-976-740-45	Sequence 45, App1
16	58	100.0	1614	13	US-10-671-242-45	Sequence 45, App1
17	58	100.0	1614	13	US-10-023-529-45	Sequence 45, App1
18	58	100.0	1614	13	US-10-023-523-45	Sequence 45, App1
19	58	100.0	1614	15	US-10-616-187-45	Sequence 45, App1
20	58	100.0	12425	9	US-09-976-740-50	Sequence 50, App1
21	58	100.0	12425	12	US-10-671-242-50	Sequence 50, App1
22	58	100.0	12425	13	US-10-023-529-50	Sequence 50, App1
23	58	100.0	12425	13	US-10-023-523-50	Sequence 50, App1
24	58	100.0	12425	15	US-10-616-187-50	Sequence 50, App1
25	54	93.1	1362	9	US-09-962-055-12	Sequence 12, App1
26	54	93.1	1362	9	US-09-976-740-12	Sequence 12, App1
27	54	93.1	1362	12	US-10-671-242-12	Sequence 12, App1
28	54	93.1	1362	13	US-10-023-529-12	Sequence 12, App1
29	54	93.1	1362	13	US-10-023-523-12	Sequence 12, App1
30	54	93.1	1362	15	US-10-616-187-12	Sequence 12, App1
31	54	93.1	1422	9	US-09-962-055-13	Sequence 13, App1
32	54	93.1	1422	9	US-09-976-740-13	Sequence 13, App1
33	54	93.1	1422	12	US-10-671-242-13	Sequence 13, App1
34	54	93.1	1422	13	US-10-023-529-13	Sequence 13, App1
35	54	93.1	1422	13	US-10-023-523-13	Sequence 13, App1
36	54	93.1	1422	15	US-10-616-187-13	Sequence 13, App1
37	54	93.1	1617	9	US-09-962-055-11	Sequence 11, App1
38	54	93.1	1617	9	US-09-976-740-11	Sequence 11, App1
39	54	93.1	1617	12	US-10-671-242-11	Sequence 11, App1
40	54	93.1	1617	13	US-10-023-529-11	Sequence 11, App1
41	54	93.1	1617	13	US-10-023-523-11	Sequence 11, App1
42	54	93.1	1617	15	US-10-616-187-11	Sequence 11, App1
43	54	93.1	2561	9	US-09-976-740-48	Sequence 48, App1
44	54	93.1	2561	12	US-10-671-242-48	Sequence 48, App1
45	54	93.1	2561	13	US-10-023-529-48	Sequence 48, App1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-962-055-33
Sequence 33, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
           Lees, Robert S.
           Law, Simon W.
           Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
           BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
           TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...30
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-962-055-33

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db   1 GAGGATGATGACCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x US-09-962-055-33 (1-30)

Alignment Scores:
Pred. No.:   0.00149
Score: 58.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9

Length: 30
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

RESULT 2
US-09-976-740-33
; Sequence 33, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-740-33

; SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997

Alignment Scores:
Pred. No.:   0.00149
Score: 58.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9

Length: 30
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

RESULT 3
US-10-671-242-33
; Sequence 33, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-671-242-33

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db   1 GAGGATGATGACCCGATGGCTTCTTAGGC 30

US-09-976-740-22 (1-10) x US-10-671-242-33 (1-30)

Alignment Scores:
Pred. No.:   0.00149
Score: 58.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 12

Length: 30
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

RESULT 4
US-10-023-529-33
; Sequence 33, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS

```
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 33
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-33

Alignment Scores:
Pred. No.:                0.00149        Length:         30
Score:                    58.00          Matches:        10
Percent Similarity:       100.00%        Conservative:   0
Best Local Similarity:    100.00%        Mismatches:     0
Query Match:              13             Indels:         0
DB:                                      Gaps:           0

US-09-976-740-22 (1-10) x US-10-023-529-33 (1-30)

Qy  1 GluAspAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||
Db  1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

RESULT 5
US-10-023-523-33
Sequence 33, Application US/10023523
Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Arjona, Anibal A.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 33
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-523-33

Alignment Scores:
Pred. No.:                0.00149        Length:        30
Score:                    58.00          Matches:       10
Percent Similarity:       100.00%        Conservative:  0
Best Local Similarity:    100.00%        Mismatches:    0
```

```
Query Match:              100.00%        Indels:        0
DB:                       13             Gaps:          0

US-09-976-740-22 (1-10) x US-10-023-523-33 (1-30)

Qy  1 GluAspAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||
Db  1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

RESULT 6
US-10-616-187-33
Sequence 33, Application US/10616187
Publication No. US20040013668A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Arjona, Anibal A.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 33
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-187-33

Alignment Scores:
Pred. No.:                0.00149        Length:        30
Score:                    58.00          Matches:       10
Percent Similarity:       100.00%        Conservative:  0
Best Local Similarity:    100.00%        Mismatches:    0
Query Match:              15             Indels:        0
DB:                                      Gaps:          0

US-09-976-740-22 (1-10) x US-10-616-187-33 (1-30)

Qy  1 GluAspAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||
Db  1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30

RESULT 7
US-09-962-055-16
Sequence 16, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Arjona, Anibal A.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
       TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
```

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-Nov-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-962-055-16

Alignment Scores:
Pred. No.:
Score: 0.0557   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                            9   Gaps: 0

US-09-962-055-16

Qy   1 GluAspAspProAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||||
     622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
Db

RESULT 8
US-09-976-740-16
Sequence 16, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-09-976-740-16

Alignment Scores:
Pred. No.:
Score: 0.0557   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                            9   Gaps: 0

US-09-976-740-16

Qy   1 GluAspAspProAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||||
     622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
Db

RESULT 9
US-10-671-242-16
Sequence 16, Application US/10/671242
Publication No. US20040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-10-671-242-16

Alignment Scores:
Pred. No.:
Score: 0.0557   Length: 1208
Percent Similarity: 58.00   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                            12   Gaps: 0

US-10-671-242-16

Qy   1 GluAspAspProAspProAspGlyPheLeuGly 10
       |||||||||||||||||||||||||||||||
     622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
Db

RESULT 10
US-10-023-529-16
; Sequence 16, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-529-16

Alignment Scores:
Pred. No.:
Score: 0.0557
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13

Length: 1208
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-10-023-529-16 (1-1208)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
         |||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 11
US-10-023-523-16
; Sequence 16, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-523-16

Alignment Scores:
Pred. No.:
Score: 0.0557
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13

Length: 1208
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-10-023-523-16 (1-1208)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
         |||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 12
US-10-616-187-16
; Sequence 16, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-616-187-16

Alignment Scores:
Pred. No.:
Score: 0.0557
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 15

Length: 1208
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-10-616-187-16 (1-1208)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
         |||||||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 13
US-10-102-806-247
; Sequence 247, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a, t, g, or c
; NAME/KEY: misc_feature
; LOCATION: (1336)
; OTHER INFORMATION: n equals a, t, g, or c
US-10-102-806-247

Qy   1 GluAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||
Db   622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651

Alignment Scores:
Pred. No.:
Score: 0.0615
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
US-10-102-806-247

Length: 1336
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-10-102-806-247 (1-1336)

RESULT 14
US-09-945-527-6
; Sequence 6, Application US/09945527
; Publication No. US20030055588A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid and Protein Homologs
; FILE REFERENCE: 35800/237985
; CURRENT APPLICATION NUMBER: US/09/945,527
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-945-527-6

Alignment Scores:
Pred. No.:
Score: 0.0664
Percent Similarity: 58.00
US-09-945-527-6

Length: 1445
Matches: 10
Conservative: 0

US-20030055588A1e1 Nucleic Acid Molecules Encoding

Qy   1 GluAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||
Db   694 GAGGATGATGACCCCGATGGCTTCTTAGGC 723

US-09-976-740-22 (1-10) x US-09-945-527-6 (1-1445)

Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 10   Gaps: 0

RESULT 15
US-09-976-740-45
; Sequence 45, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-976-740-45

Qy   1 GluAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||
Db   807 GAGGATGATGACCCCGATGGCTTCTTAGGC 836

Alignment Scores:
Pred. No.:
Score: 0.0741
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:

Length: 1614
Matches: 10
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-09-976-740-45 (1-1614)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||
Db   1585 GAGGATGATGACCCCGATGGCTTCTTAGGC 1614

Search completed: March 13, 2004, 04:26:15
Job time : 15.4676 secs

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:        March 12, 2004, 19:55:37 ; Search time 151.2 Seconds
                                           (without alignments)
                                           1975.018 Million cell updates/sec

Title:         US-09-976-740-22
Perfect score: 58
Sequence:      1 EDDPDGFLG 10

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      27513289 seqs, 1491090276 residues

Total number of hits satisfying chosen parameters:    55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-O=/ccgn2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1_10232_@runat_10032004_094548_19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  EST:*
        1: em_estba:*
        2: em_esthum:*
        3: em_estin:*
        4: em_estmu:*
        5: em_estov:*
        6: em_estpl:*
        7: em_estro:*
        8: em_htc:*
        9: em_est1:*
       10: gb_est2:*
       11: gb_htc:*
       12: gb_est3:*
       13: gb_est4:*
       14: gb_est5:*
       15: em_estom:*
       16: em_estfun:*
       17: em_estba_hum:*
       18: em_gss_inv:*
       19: em_gss_pln:*
       20: em_gss_vrt:*
       21: em_gss_fun:*
       22: em_gss_mam:*
       23: em_gss_mus:*
       24: em_gss_rod:*
       25: em_gss_pro:*
       26: em_gss_phg:*
       27: em_gss_vrl:*
       28: gb_gss1:*
       29: gb_gss2:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB ID	Description
1	58	100.0	313	9	AA481593	AA481593 aa35e06.r
2	58	100.0	361	14	D80440	HUM074C06A
3	58	100.0	362	9	AA311602	EST182332
4	58	100.0	406	12	BP432333	BP432333
5	58	100.0	411	14	CB802479	AMGNNUC:S
6	58	100.0	427	13	AI247702	qh60h02.x
7	58	100.0	430	13	BQ317482	RC1-CT030
8	58	100.0	436	9	AI057236	oz11d06.x
9	58	100.0	454	9	AI198288	qi61d04.x
10	58	100.0	454	9	AI498877	tm68h04.x
11	58	100.0	457	12	BM714074	UI-E-EJ0-
12	58	100.0	461	12	BM675258	UI-E-EJ0-
13	58	100.0	464	12	BM842690	K-EST0120
14	58	100.0	464	12	BM842726	K-EST0120
15	58	100.0	466	12	BM840318	K-EST0117
16	58	100.0	469	14	R76498	R76498 yi61e11.r1
17	58	100.0	490	10	AI271358	qi03d11.x
18	58	100.0	491	10	BE696235	RC1-CT030
19	58	100.0	537	12	BI838958	60308925
20	58	100.0	538	14	CB717489	AMGNNUC:N
21	58	100.0	557	14	CD673768	fs04b02.y
22	58	100.0	558	12	BG827200	60749308
23	58	100.0	611	10	BF334560	RC1-CT030
24	58	100.0	611	12	BI114110	60286292
25	58	100.0	632	12	AW861194	RC1-CT030
26	58	100.0	663	12	BX118116	BX118116
27	58	100.0	692	13	BG825632	60274981
28	58	100.0	699	12	BG190740	UI-R-DZ0-
29	58	100.0	709	13	BQ196255	UI-R-DZ0-
30	58	100.0	711	13	BQ200548	UI-R-DZ1-
31	58	100.0	736	13	BQ031920	UI-R-DZ1-
32	58	100.0	748	10	BM013469	60306712
33	58	100.0	756	13	BM031469	60638922
34	58	100.0	764	13	BQ445960	UI-H-EU1-
35	58	100.0	780	14	CB325238	UI-R-DZ0-
36	58	100.0	785	14	BI226646	60951660
37	58	100.0	795	14	CB324552	UI-H-FL1-
38	58	100.0	799	12	BU620639	UI-H-FL1-
39	58	100.0	812	12	BG762763	60273678
40	58	100.0	829	10	BE270987	60943804
41	58	100.0	862	13	BQ673964	AGENCOURT
42	58	100.0	1109	10	BE270805	60094380
43	54	93.1	461	12	BI305052	AR068D101
44	54	93.1	534	12	AW669983	113563 MA
45	53	91.4	592	12	BI343168	371223 MA
			255	13	BQ084241	K-EST0148

29: gb_gss2:*

ALIGNMENTS

RESULT 1
AA481593/c

```
LOCUS       AA481593      313 bp   mRNA    linear   EST 14-AUG-1997
DEFINITION  aa35e06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815266 5',
            mRNA sequence.
ACCESSION   AA481593
VERSION     AA481593.1  GI:2211145
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 313)
```

```
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE      Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbe-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., David Allman,
           Ph.D., Gerald Marti, M.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Seq primer: -28m13 rev1 ET from Amersham
           High quality sequence stop: 212.

FEATURES             Location/Qualifiers
     source          1..313
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:6034339"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:815266"
                     /tissue_type="germinal center B cell"
                     /clone_lib="NCI_CGAP_GC81"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAGTCGGGAGCGGCCGCCCGCTCAATTTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-22 (1-10) x AA481593 (1-313)

Alignment Scores:
Pred. No.:              1.99
Score:                 58.00
Percent Similarity:   100.00%        Length:         313
Best Local Similarity: 100.00%       Matches:         10
Query Match:          100.00%        Conservative:     0
DB:                        9         Mismatches:       0
                                     Indels:           0
                                     Gaps:             0

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 252 GAGGAGGATGACCCGATGGCTTCTTAGGC 223


RESULT 2
LOCUS       D80440                   361 bp    mRNA    linear   EST 09-FEB-1996
DEFINITION  HUM074C06A Human fetal brain (TFujiwara) Homo sapiens cDNA clone
            GEN-074C06 3', mRNA sequence.
ACCESSION   D80440
VERSION     D80440.1  GI:1178317
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 361)
  AUTHORS   Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,P., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
  TITLE     Fujiwara et al. (1995)
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co., Ltd
            463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
            Tel: 0886-65-2888
            Fax: 0886-37-1035.

FEATURES             Location/Qualifiers
     source          1..361
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /db="GEN-074C06"
                     /clone="GEN-074C06"
                     /dev_stage="fetal"
                     /clone_lib="Human fetal brain (TFujiwara)"
                     /note="Organ: brain"

ORIGIN

US-09-976-740-22 (1-10) x D80440 (1-361)

Alignment Scores:
Pred. No.:              2.34
Score:                 58.00
Percent Similarity:   100.00%        Length:         361
Best Local Similarity: 100.00%       Matches:         10
Query Match:          100.00%        Conservative:     0
DB:                       14         Mismatches:       0
                                     Indels:           0
                                     Gaps:             0

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
       ||||||||||||||||||||||||||||||
Db 284 GAGGAGGATGACCCGATGGCTTCTTAGGC 255


RESULT 3
LOCUS       AA311602                 362 bp    mRNA    linear   EST 19-APR-1997
DEFINITION  EST182332 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
            sequence.
ACCESSION   AA311602
VERSION     AA311602.1  GI:1963931
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,H.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC122721
            Contact: Kerlavage,AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
```

```
             Tel: 3018699056
             Fax: 3018699423
             Email: arkerlav@tigr.org
             For clone availability, additional sequence and expression
             information related to this EST, please check the TIGR Human Gene
             Index (http://www.tigr.org/tdb/hgi/hgi.html)
             Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .362
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /cell_type="T-lymphocyte"
                      /clone_lib="Jurkat T-cells VI"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
ORIGIN

US-09-976-740-22 (1-10) x AA311602 (1-362)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
        |||||||||||||||||||||||||||
Db 305 GAGGAGGATGATGACCCCGATGGCTTCTTAGGC 334

Alignment Scores:
Pred. No.:
Score:                   2.34            Length:        362
Percent Similarity:      58.00           Matches:        10
Best Local Similarity:   100.00%         Conservative:    0
Query Match:             100.00%         Mismatches:      0
DB:                      9               Indels:          0
                                         Gaps:            0


RESULT 4
BP432333
BP432333
LOCUS       BP432333        406 bp    mRNA    linear    EST 09-SEP-2003
DEFINITION  BP432333 leukemia cell normalized cDNA library Homo sapiens cDNA
            clone LEU4076_8_D5, mRNA sequence.
ACCESSION   BP432333
VERSION     BP432333.1     GI:34555032
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 406)
AUTHORS     Takagaki,K., Katsuma,S., Horio,T., Kaminishi,Y., Hada,Y.,
            Tanaka,T., Ohgi,T. and Yano,J.
TITLE       cDNA microarray analysis of altered gene expression in
            Ara-C-treated leukemia cells
JOURNAL     Biochem. Biophys. Res. Commun. 309 (2), 351-358 (2003)
MEDLINE     22831100
PUBMED      12951057
COMMENT     Contact: Kazuchika Takagaki
            Research Laboratories
            Nippon Shinyaku Co. Ltd.
            Sakura 3-14-1, Tsukuba, Ibaraki 305-0003, Japan
            Tel: 81-29-850-6242
            Fax: 81-29-850-6217
            Email: k.takagaki@nippon-shinyaku.co.jp.
FEATURES              Location/Qualifiers
     source           1. .406
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="LEU4076_8_D5"
                      /cell_type="leukemia cell"
                      /clone_lib="leukemia cell normalized cDNA library"
                      /note="mRNA expressed in leukemia cells (mixture of
                      CCRF-CEM, K562, HL-60, MOLT-4, or RPMI-8226)"
ORIGIN

Alignment Scores:

US-09-976-740-22 (1-10) x BP432333 (1-406)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
        |||||||||||||||||||||||||||
Db 246 GAGGAGGATGATGACCCCGATGGCTTCTTAGGC 275

Alignment Scores:
Pred. No.:
Score:                   2.67            Length:        406
Percent Similarity:      58.00           Matches:        10
Best Local Similarity:   100.00%         Conservative:    0
Query Match:             100.00%         Mismatches:      0
DB:                      12              Indels:          0
                                         Gaps:            0


RESULT 5
CB802479
CB802479
LOCUS       CB802479        411 bp    mRNA    linear    EST 16-MAY-2003
DEFINITION  AWGNNUC:SRPB2-00295-B1-A srpb2 (10220) Rattus norvegicus cDNA clone
            srpb2-00295-b1 5', mRNA sequence.
ACCESSION   CB802479
VERSION     CB802479.1     GI:29916753
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 411)
AUTHORS     Amgen EST Program
TITLE       Amgen Rat EST Program
JOURNAL     Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00295  row: b  column: 1.
FEATURES              Location/Qualifiers
     source           1. .411
                      /organism="Rattus norvegicus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10116"
                      /clone="srpb2-00295-b1"
                      /tissue_type="prostate tissue"
                      /clone_lib="srpb2 (10220)"
                      /note="Vector: PSPORT1; Site_1: SalI; Site_2: NotI; rat
                      prostate normalized double selected poly(A+) mRNA size
                      fraction > 1 kb"
ORIGIN

US-09-976-740-22 (1-10) x CB802479 (1-411)

Qy   1 GluAspAspProAspGlyPheLeuGly 10
        |||||||||||||||||||||||||||
Db 184 GAGGACGATGATGATCCTGATGGCTTCTTAGGC 213

Alignment Scores:
Pred. No.:
Score:                   2.7             Length:        411
Percent Similarity:      58.00           Matches:        10
Best Local Similarity:   100.00%         Conservative:    0
Query Match:             100.00%         Mismatches:      0
DB:                      14              Indels:          0
                                         Gaps:            0


RESULT 6
AI247702
AI247702/c
LOCUS       AI247702        427 bp    mRNA    linear    EST 01-DEC-1998
DEFINITION  qh60h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo
            sapiens cDNA
            clone IMAGE:1849107 3' similar to TR:P78365 P78365 POLYHOMEOTIC 2
            HOMOLOG. ;, mRNA sequence.
ACCESSION   AI247702
VERSION     AI247702.1     GI:3843099
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 427)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 349.
FEATURES             Location/Qualifiers
     source          1..427
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1849107"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library. 1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5',
                     AACTGGAAGAAATTAAATTAAAGACTCTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia) digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

US-09-976-740-22 (1-10) x AI247702 (1-427)

Alignment Scores:
 Pred. No.:
 Score:                  2.82                Length:        427
 Percent Similarity:    58.00     Matches:        10
 Best Local Similarity: 100.00%   Conservative:    0
 Query Match:           100.00%   Mismatches:      0
                        9         Indels:          0
 DB:                              Gaps:            0

Qy    1 GluAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||
Db  289 GAGGATGATGATGACCCGATGGCTTCTTAGGC 260

RESULT 7
BQ317482
LOCUS       BQ317482  430 bp  mRNA  linear  EST 17-MAY-2002
DEFINITION  RC1-CT0302-040400-017-d09 CT0302 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ317482
VERSION     BQ317482.1  GI:20923251
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 430)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.,Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
```

```
PUBMED   10737800
COMMENT  Contact: Simpson A.J.G.
         Laboratory of Cancer Genetics
         Ludwig Institute for Cancer Research
         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
         Brazil
         Tel: +55-11-2704922
         Fax: +55-11-2707001
         Email: asimpson@ludwig.org.br
         This sequence was derived from the FAPESP/LICR Human Cancer Genome
         Project. This entry can be seen in the following URL
         (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1-CT0302-
         040400-017-d09&t3=2000-04-04&t4=1)
FEATURES             Location/Qualifiers
     source          1..430
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0302"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No.
                     196,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

US-09-976-740-22 (1-10) x BQ317482 (1-430)

Alignment Scores:
 Pred. No.:
 Score:                  2.84                Length:        430
 Percent Similarity:    58.00     Matches:        10
 Best Local Similarity: 100.00%   Conservative:    0
 Query Match:           100.00%   Mismatches:      0
                        13        Indels:          0
 DB:                              Gaps:            0

Qy    1 GluAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||
Db  144 GAGGATGATGATGACCCGATGGCTTCTTAGGC 173

RESULT 8
AI057236
AI057236/c
LOCUS       AI057236  436 bp  mRNA  linear  EST 29-SEP-1998
DEFINITION  oz11d06.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1675019 3' similar to TR:P78365 P78365 POLYHOMEOTIC 2
            HOMOLOG.  ;, mRNA sequence.
ACCESSION   AI057236
VERSION     AI057236.1  GI:3331102
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 436)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 593   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 351.
FEATURES             Location/Qualifiers
     source          1..436
                     /organism="Homo sapiens"
```

RESULT 9

```
LOCUS       AI198288                   454 bp    mRNA    linear   EST 02-DEC-1998
DEFINITION  qi61d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860967 3'
            similar to TR:P78365 P78365 POLYHOMEOTIC 2 HOMOLOG. ;, mRNA
            sequence.
ACCESSION   AI198288
VERSION     AI198288.1  GI:3750894
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 685   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 374.
FEATURES             Location/Qualifiers
     source          1..454
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1860967"
```

US-09-976-740-22 (1-10) x AI057236 (1-436)

Alignment Scores:
Pred. No.:
Score: 2.89
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 100.00%
                              9

```
                    Length:        436
                    Matches:       10
                    Conservative:  0
                    Mismatches:    0
                    Indels:        0
                    Gaps:          0
```

ORIGIN

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
          |||||||||||||||||||||||||||||||
Db 289 GAGGATGATGACCCCGATGGCTTCTTAGGC 260

RESULT 10

```
LOCUS       AI498877                   454 bp    mRNA    linear   EST 14-APR-1999
DEFINITION  tm68h04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163319 3'
            similar to TR:P78365 P78365 POLYHOMEOTIC 2 HOMOLOG. ;, mRNA
            sequence.
ACCESSION   AI498877
VERSION     AI498877.1  GI:4350859
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 698   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 372.
FEATURES             Location/Qualifiers
     source          1..454
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2163319"
                     /tissue_type="anaplastic oligodendroglioma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Brn25"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCGAAGTCGGACGCGGCCGCCATAGGTTTTTTTTTTTTTTTTTTTT
                     T 3'], double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
```

US-09-976-740-22 (1-10) x AI198288 (1-454)

Alignment Scores:
Pred. No.:
Score: 3.02
Percent Similarity: 58.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 100.00%
                              9

```
                    Length:        454
                    Matches:       10
                    Conservative:  0
                    Mismatches:    0
                    Indels:        0
                    Gaps:          0
```

ORIGIN

Qy   1 GluAspAlaAspProAspGlyPheLeuGly 10
          |||||||||||||||||||||||||||||||
Db 301 GAGGATGATGACCCCGATGGCTTCTTAGGC 272

RESULT 11

ORIGIN

TGTTACCAAGTCGAAGTGGAGGACGGGGCGCCCATAGGTTTTTTTTTTTTTTTTTTTTTTT
T3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

Alignment Scores:

Pred. No.:   3.02
Score: 58.00   Length: 454
Percent Similarity: 100.00%   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                   Gaps: 0

US-09-976-740-22 (1-10) x A1498877 (1-454)

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
          ||||||||||||||||||||||||||||||
Db   301 GAGGATGATGACCCCGATGGCTTCTTAGGC 272

LOCUS   BM714074   457 bp   mRNA   linear   EST 28-FEB-2002
DEFINITION UI-E-EJO-ahr-h-07-0-UI.r1 UI-E-EJO Homo sapiens cDNA clone
            UI-E-EJO-ahr-h-07-0-UI 5', mRNA sequence.
ACCESSION   BM714074
VERSION   BM714074.1 GI:19027332
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 457)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES   Location/Qualifiers
     source   1..457
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJO-ahr-h-07-0-UI"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EJO"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-E-EJO is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double

RESULT 12

ORIGIN

stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGGGA; eye anterior segment,
AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."

Alignment Scores:

Pred. No.:   3.05
Score: 58.00   Length: 457
Percent Similarity: 100.00%   Matches: 10
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 12   Indels: 0
                                   Gaps: 0

US-09-976-740-22 (1-10) x BM714074 (1-457)

Qy   1 GluAspAspAspProAspGlyPheLeuGly 10
          ||||||||||||||||||||||||||||||
Db   149 GAGGATGATGACCCCGATGGCTTCTTAGGC 178

LOCUS   BM675258   461 bp   mRNA   linear   EST 27-FEB-2002
DEFINITION UI-E-EJO-ahr-h-07-0-UI.s1 UI-E-EJO Homo sapiens cDNA clone
            UI-E-EJO-ahr-h-07-0-UI 3', mRNA sequence.
ACCESSION   BM675258
VERSION   BM675258.1 GI:18985156
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 461)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=yes.
FEATURES   Location/Qualifiers
     source   1..461
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJO-ahr-h-07-0-UI"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EJO"

RESULT 13

```
BM842690
LOCUS       BM842690                 464 bp    mRNA    linear      EST 06-MAR-2002
DEFINITION  K-EST0120140 S12SNU216 Homo sapiens cDNA clone S12SNU216-68-F06 5',
            mRNA sequence.
ACCESSION   BM842690
VERSION     BM842690.1  GI:19199099
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 464)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 68 row: F column: 06
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
     source          1..464
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-68-F06"
                     /sex="F"
                     /tissue_type="Lymph node"
                     /cell_type="Epithelial"
                     /cell_line="SNU-216"
```

ORIGIN

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AATGGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
AGAATCAAGA; lens, CGATTAGGCA; eye anterior segment,
AGAATCAAGA; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
TAG_TISSUE=human retina
TAG_LIB=UI-E-EJO
TAG_SEQ=CCGCG"

Qy 1 GluAspAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||||||||||
Db 304 GAGGATGATGACCCCGATGGCTTCTTAGGC 275

US-09-976-740-22 (1-10) x BM675258 (1-461)

Alignment Scores:
Pred. No.:   3.08
Score: 58.00
Percent Similarity: 100.00%   Length: 461
Best Local Similarity: 100.00%   Matches: 10
Query Match: 100.00%   Conservative: 0
DB: 12   Mismatches: 0
                                    Indels: 0
                                    Gaps: 0

RESULT 14

```
BM842726
LOCUS       BM842726                 464 bp    mRNA    linear      EST 06-MAR-2002
DEFINITION  K-EST0120184 S12SNU216 Homo sapiens cDNA clone S12SNU216-66-B02 5',
            mRNA sequence.
ACCESSION   BM842726
VERSION     BM842726.1  GI:19199135
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 464)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 66 row: B column: 02
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
     source          1..464
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-66-B02"
                     /sex="F"
                     /tissue_type="Lymph node"
                     /cell_type="Epithelial"
                     /cell_line="SNU-216"
                     /lab_host="Top10F'"
                     /clone_lib="S12SNU216"
```

ORIGIN

/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
/clone_lib="S12SNU216"
/lab_host="Top10F'"
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesied from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

Qy 1 GluAspAspAspProAspGlyPheLeuGly 10
      |||||||||||||||||||||||||||||||
Db 249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278

US-09-976-740-22 (1-10) x BM842690 (1-464)

Alignment Scores:
Pred. No.:   3.1
Score: 58.00
Percent Similarity: 100.00%   Length: 464
Best Local Similarity: 100.00%   Matches: 10
Query Match: 100.00%   Conservative: 0
DB: 12   Mismatches: 0
                                    Indels: 0
                                    Gaps: 0

```
ORIGIN
        bacterial alkaline phosphatase (BAP) and then decapped
        with tobacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including EcoR
        I site by treatment of T4 RNA ligase and the first strand
        cDNA was synthesized from oligo dT-selected mRNA by
        priming with dT-tailed vector. The dT-tailed vector was
        adjusted to have about 60nt. The cDNA ligase after digestion of
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10F' by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."

Alignment Scores:
Pred. No.:              3.11
Score:                  58.00                Length:          466
Percent Similarity:     100.00%              Matches:         10
Best Local Similarity:  100.00%              Conservative:    0
Query Match:            100.00%              Mismatches:      0
DB:                                          Indels:          0
                        12                   Gaps:            0

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db  249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278

US-09-976-740-22 (1-10) x BM840318 (1-466)

Search completed: March 13, 2004, 04:01:47
Job time : 157.2 secs
```

```
RESULT 15
BM840318
LOCUS       BM840318                      466 bp     mRNA       linear       EST 06-MAR-2002
DEFINITION  K-EST0117357 S12SNU216 Homo sapiens cDNA clone S12SNU216-41-E05 5'',
            mRNA sequence.
ACCESSION   BM840318
VERSION     BM840318.1   GI:19196727
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 41 row: E column: 05
            High quality sequence stop: 466.
FEATURES             Location/Qualifiers
     source          1..466
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-41-E05"
                     /sex="F"
                     /tissue_type="lymph node"
                     /cell_type="Epithelial"
                     /cell_line="SNU-216"
                     /lab_host="Top10F'"
                     /clone_lib="S12SNU216"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
```

```
ORIGIN
        /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
        Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
        bacterial alkaline phosphatase (BAP) and then decapped
        with tobacco acid pyrophosphatase (TAP). The decapped
        intact mRNA was ligated with DNA-RNA linker including EcoR
        I site by treatment of T4 RNA ligase and the first strand
        cDNA was synthesized from oligo dT-selected mRNA by
        priming with dT-tailed vector. The cDNA ligase after digestion of
        adjusted to have about 60nt. The dT-tailed vector was
        circularized with E. coli DNA ligase after digestion of
        EcoRI which site is also included in vector. An RNA strand
        converted to a DNA strand by Okayama-Berg method. The
        obtained cDNA vectors were used for transformation of
        competent cells E. coli Top10F' by electroporation method.
        The cDNA libraries constructed by this method are
        full-length enriched cDNA library."

Alignment Scores:
Pred. No.:              3.1
Score:                  58.00                Length:          464
Percent Similarity:     100.00%              Matches:         10
Best Local Similarity:  100.00%              Conservative:    0
Query Match:            100.00%              Mismatches:      0
DB:                                          Indels:          0
                        12                   Gaps:            0

US-09-976-740-22 (1-10) x BM842726 (1-464)

Qy    1 GluAspAspAspProAspGlyPheLeuGly 10
        ||||||||||||||||||||||||||||||
Db  249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278
```

To Check Priority date (handwritten)

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:48:14 ; Search time 343.96 Seconds
(without alignments)
2680.137 Million cell updates/sec

Title: US-09-976-740-7
Perfect score: 1170
Sequence: 1 EERVLEKEEEDDDEDEDEE.........HIKVLQQGHFEDDDPDGPLG 217

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USR=US09976740 @CGN 1 1 1596 @runat 10032004 094547 19532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1170	100.0	1208	2	AAV32838	Aav32838 Human low
2	1170	100.0	1208	2	AAH26494	Aah26494 Human low
3	1170	100.0	1614	5	AAH26499	Aah26499 Human low
4	1161	99.2	1336	3	AAF21860	Aaf21860 Human bre
5	1047.5	89.5	1362	5	AAH26489	Aah26489 Rabbit lo
6	1047.5	89.5	1422	5	AAH26490	Aah26490 Rabbit lo
7	1047.5	89.5	1617	5	AAH26488	Aah26488 Rabbit lo
8	1047.5	89.5	2561	5	AAH26500	Aah26500 Rabbit lo
c 10	1041.5	89.0	1617	2	AAV32835	Aav32835 Rabbit lo
c 11	1036.5	88.6	1242	5	AAH26495	Aah26495 Human low
c 12	811	69.3	1134	3	AAC59574	Aacs9574 Human sec
c 13	451	38.5	460	9	ADB49888	Adb49888 Primary r
14	305.5	26.1	1566	7	ADA53650	Adas3650 Human cod
15	300	25.6	1957	6	ABA91317	Aba91317 Human col
16	285	24.4	483	5	AAS75500	Aas75500 DNA encod
17	285	24.4	1066	5	ABA83039	Aba83039 Human pol
18	285	24.4	1598	4	AAI60534	Aai60534 Human pol
19	285	24.4	1601	8	AAI58748	Aai58748 Human pol
20	284	24.3	1402	6	ABZ57768	Abz57768 Human cel
21	187.5	16.0	892	6	ADE59157	Ade59157 Human gen
22	174	14.9	2570	6	AAS94834	Aas94834 Human DNA
23	174	14.9	2799	7	ADA19295	Ada19295 Human ins
24	174	14.9	2800	7	ADA53340	Adas3340 Human cod
25	170.5	14.6	3396	6	ABZ11784	Abz11784 Human pol
26	170.5	14.6	4220	7	ABZ20383	Abz20383 Oncofoeta
27	170.5	14.6	7921	7	ACC47332	Acc47332 Human pro
28	169	14.4	1718	4	AAH33518	Aah33518 Human col
29	169	14.4	3109	6	ABN59907	Abn59907 Novel hum
30	168.5	14.4	1933	2	AAV36953	Aav36953 Human pol
31	168.5	14.4	1933	2	AAV34954	Aav34954 Homo sapi
32	167	14.3	3620	5	AAH89897	Aah89897 Human bon
33	162.5	13.9	1402	5	ABL04955	Abl04955 Drosophil
34	162.5	13.9	2081	8	ACA99934	Aca99934 cDNA enco
35	162.5	13.9	3970	4	ABL04954	Abl04954 Drosophil
36	162.5	13.2	3065	2	AAV00010	Aav00010 Mouse sex
37	154.5	13.2	3065	2	AAV00014	Aav00014 Mouse sex
38	154.5	13.2	3065	2	AAX61316	Aax61316 Mouse Scm
39	153.5	13.1	2277	9	ADB63579	Adb63579 Human cDN
40	153	13.1	2714	2	AAX27922	Aax27922 Mouse 1(3
41	153	13.1	3879	2	AAV29009	Aav29009 Human pol
42	153	13.1	3879	2	AAV21060	Aav21060 cDNA enco
43	153	12.9	6525	9	ADE53749	Ade53749 DNA encod
44	151.5	12.9	676	5	AAS85220	Aas85220 DNA encod
45	151.5	12.9	681	5	AAS88059	Aas88059 DNA encod

ALIGNMENTS

RESULT 1
AAV32838

ID   AAV32838 standard; cDNA; 1208 BP.
XX
AC   AAV32838;
XX
DT   09-NOV-1998 (first entry)
XX
DE   Human low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW   receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   1..654
FT   /tag= a
FT   misc_feature   22..99
FT   /tag= c
FT   /note= "Claim 13"
FT   misc_feature   22..66
FT   /tag= b
FT   /note= "Claim 12"
FT   misc_feature   67..99
FT   /tag= d
FT   /note= "Claim 14"
FT   misc_feature   622..651
FT   /tag= e
FT   /note= "Claim 15"
XX
PN   WO9823282-A1.

XX
PD   04-JUN-1998.
XX
PF   26-NOV-1997;   97WO-US021857.
XX
PR   27-NOV-1996;   96US-0031930P.
PR   03-JUN-1997;   97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49041.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 9; Fig 16; 47pp; English.
XX
CC   This cDNA clone codes for novel human low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49041). It was isolated by screening human
CC   liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA
CC   clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
CC   42) are claimed. An abnormality in LBP metabolism or structure is
CC   diagnostic of a risk for atherosclerosis. The invention provides: methods
CC   for determining if an animal is at risk for atherosclerosis (e.g. for
CC   prenatal screening); methods for treating atherosclerosis (including gene
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

US-09-976-740-7 (1-217) x AAV32838 (1-1208)

Alignment Scores:
Pred. No.:
Score: 4.32e-60
Score: 1170.00   Length: 1208
Percent Similarity: 100.00%   Matches: 217
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 2   Indels: 0
                                        Gaps: 0

```
Qy    1 GluGluArgValLeuGlnLeuGlyLysGlnLeuAspAlaProGlySerGlyGluGlu  20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGACGGAGTACTTGAGAGAAGAGGAGGAAGAAGATGAAGATGAAGAAGAA        60

Qy   21 AspAspValSerGlyValProGlyserGlnAspAspArgProAlaGlyAlaGlnHis  40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGACGTGTCAGAGGGTCTGAAGTGCCCCGAGAGTGACCGTCCTGCAGCAC       120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGGGAGCGGGGACCTCAGAGTCCCAAGGAGAGGGTCAAGGAGTGGACC 180

Qy   61 ProCysGlyProHisGlnGlnGlyAspProAlaProGlySerGlyThr  80
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCACACCAACAGGGCCAGGATGAAGGGCCCCCCAGGGCCAGGGGCACC    240

Qy   81 ArgGlnValPheSerMetAlaAlaAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGTGTTCTCCATGGCAGCCAATGAACAAGAAGGGCAACAGCTTCGTTGCCAC    300

Qy  101 GlyProAspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GGGCCCGACTCCCCGTCCCCGGTGCCTTTGCCCCAGGGCAAAACCAGCCCTACCTG    360

Qy  121 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACGGGACCCCCTTTGGCTGTTGCTCCCCGGGCCGCAAGAGAAGGAAGCCATCTGATCCGTCGAG 420

Qy  141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TGGACCGTGATGGATGTCGTCGAATATTTACTGAGGCTGGATTCCCGAGCAGGGCGACA  480

Qy  161 AlaPheGluGlnGlnHisIleAspGlyGlysSerLeuLeuLeuMetGlnArgThrAspVal 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCTTTCCAAGAGCAGGAAAATTGATGGCAGAAATCTTTGTCTCATGCAGCGCACAGAGTG  540

Qy  181 LeuThrGlyValLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTCACCGGCGTTGCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCATCAAG   600

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspProGlyPheLeuGly 217
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTGCTTCAGCCAAGGCCACTTTGAGGATGAATGACCCGGATCCCGGATTCTTAGGC   651
```

RESULT 2
AAH26494
ID   AAH26494 standard; cDNA, 1208 BP.
XX
AC   AAH26494;
XX
DT   12-NOV-2001   (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..654
FT   /*tag= a
FT   /partial
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82803.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 4; Fig 16; 143pp; English.
XX
CC   The present sequence is that of a partial cDNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC   isolated from human foetal brain, liver and aorta cDNA libraries using
CC   rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC   AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides capable of binding to native and methylated LDL. Also
CC   claimed are isolated LBP polypeptides, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, methods for evaluating an agent for use in treating
CC   atherosclerosis, and methods for treating a cell having an abnormality in

```
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:               4.32e-60
Score:                   1170.00          Length:         1208
                                          Matches:        217
Percent Similarity:      100.00%          Conservative:   0
Best Local Similarity:   100.00%          Mismatches:     0
Query Match:             5                Indels:         0
DB:                                       Gaps:           0

US-09-976-740-7 (1-217) x AAH26494 (1-1208)

Qy     1 GluGluArgValLeuGlyLysGlyGluGlyLeuGluAspAspAspProGlyLeuAspGluGlu 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GAAGAGCGAGTACTTGAGAAAGGAGAGGGACTCAAGGAGGATCATTGATGAAGAAGATGAAGAA 60

Qy    21 AspAspAsnValSerGlyLysGluValProGlySerAspArgProAlaGlyAlaGlnHis 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GATGACGTGTCAGAGGGCTCTGAAGTGCCCGGAGTGACCCGTCCCTGCAGGTCCCAGCAC 120

Qy    41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACCAGCTTAACGGCGAGCGGGGACCTTCAGAGTGCCAAGGAGCGGGTCAAGGAGTGGACC 180

Qy    61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCTGCGGACCCCACCAGGGCCAGGATGAAGGGCGGGGGCCCGGCACCCGGCAGCGGCACC 240

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyGlyGlyThrAlaSerValAlaThr 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGGAGGGGGAGGAACCGCTTCTGTTGCCACC 300

Qy   101 GlyProAspSerProSerProProValProLeuProProGlyLysProAlaLeuProGlyAla 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCCAGACTCCCCGTCCCCGGCCTTTGCCCCAGGAAACCAGCCCTACCTGGGGGCC 360

Qy   121 AspGlyThrProHisGluGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGGGACCCCCCTTTGCGCTGTCCTCCCGGGGCCAAAGAGAAGCCACTCGATCCCGTCGAG 420

Qy   141 TrpThrValMetAspValValGluTyrPheThrGlyLeuGlyProGlyGlnAlaThr 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGACCGTGATGGATGTCGTGGAATATTTTACTGAGGGTGGACCCAGGGCAGGCCACA 480

Qy   161 AlaPheGlyGlnGlnGluIleAspGlyLysSerLeuLeuMetGlnAsnGlyThrAspVal 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTCATGCAGAACGGCACAGATGTG 540

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysSerIleTyrGluHisHisIleLys 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTCACCGGCCTGTCCATCCGGCTGGGGCCAGCCCTGAAAATCTACGAGCACCATCAAG 600

Qy   201 ValLeuGlnHisGlyHisProHisAspAspAspProGlyPheLeuGly 217
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGCTTCAGCAAGGCCACTTGAGGATGATGACCCGATGGCTTCTTAGGC 651


RESULT 3
AAH26499
ID   AAH26499 standard; DNA; 1614 BP.
XX
AC   AAH26499;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
```

```
XX
OS   Homo sapiens.
XX
PN   WO20016487 4-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Claim 7; Fig 7A; 143pp; English.
XX
CC   The present sequence is that of the coding region of the human gene (see
CC   also AAH26494) encoding novel human low density lipoprotein binding
CC   protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA
CC   library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the
CC   present sequence differs from that predicted from a cDNA clone (see
CC   AAB82803) in that it contains an additional 321 amino acids at its N-
CC   terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among
CC   claimed polynucleotides of the invention that encode novel polypeptides
CC   capable of binding to native and methylated LDL. Also claimed are
CC   isolated LBP polypeptides, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, and methods for treating a cell having an abnormality in
CC   atherosclerosis, methods for evaluating an agent for use in treating
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1614 BP; 243 A; 564 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               5.72e-60
Score:                   1170.00          Length:         1614
                                          Matches:        217
Percent Similarity:      100.00%          Conservative:   0
Best Local Similarity:   100.00%          Mismatches:     0
Query Match:             5                Indels:         0
DB:                                       Gaps:           0

US-09-976-740-7 (1-217) x AAH26499 (1-1614)

Qy     1 GluGluArgValLeuGlyLysGlyGluGlyLeuGluAspAspAspProGlyLeuAspGluGlu 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 GAAGAGCGAGTACTTGAGAAAGGAGAGGGACTCAAGGAGGATCATTGATGAAGAAGATGAAGAA 1023

Qy    21 AspAspAsnValSerGlyLysGluValProGlySerAspArgProAlaGlyAlaGlnHis 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 GATGACGTGTCAGAGGGCTCTGAAGTGCCCGGAGTGACCCGTCCCTGCAGGTCCCAGCAC 1083

Qy    41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1084 CACCAGCTTAACGGCGAGCGGGGACCTTCAGAGTGCCAAGGAGCGGGTCAAGGAGTGGACC 1143

Qy    61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1144 CCCTGCGGACCCCACCAGGGCCAGGATGAAGGGCGGGGGCCCGGCACCCGGCAGCGGCACC 1203

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyGlyGlyThrAlaSerValAlaThr 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGGAGGGGGAGGAACCGCTTCTGTTGCCACC 1263
```

RESULT 4
AAF21860

```
Qy   101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1264 GGGCCAGACTCCCCCTCGCCCGTGCCTTTCCCCCCAGGGAAACCAAGCCCTTACCTGGGGGC 1323

Qy   121 AspGlyThrProPheGlyCysProProGlyAlaArgLysGlySerAspSerAspProValGlu 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1324 GACGGGACCCCCTTTGGCTGTCCGCCCGGGGCGCAAAGAGGAAGCCATCTGATCCGGTCGAG 1383

Qy   141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPhePheProGlnGlnAlaThr 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1384 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA 1443

Qy   161 AlaPheGlnGlnGlnGlnIleAspSerLeuLeuLeuMetGlnArgThrAspVal 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1444 GCTTTCCAAGAGCAGGAAAATTGATGGTCGTCAGCCACCAGAGTGTG 1503

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1504 CTCACCGGGCCTGTCCATCCGCCCTTGAAAATCTACGAGCACCACATCAAG 1563

Qy   201 ValLeuGlnLnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1564 GTGCTTCAGCAAGGCCACTTTGAGGATGACCCGATGGCTTCTTAGGC 1614
```

ID   AAF21860 standard; DNA; 1336 BP.
XX
AC   AAF21860;
XX
DT   27-MAR-2001 (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 247.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005881.
XX
PR   12-MAR-1999; 99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58957.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these gene, useful in the prevention, treatment
PT   and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT   neurological diseases.
XX
PS   Claim 1; Page 670-671; 1299pp; English.
CC
CC   Sequences AAF21614 - AAF220031 represent DNA sequences encoding human
CC   proteins AAB59711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemias; wound healing;
CC   neurological diseases such as cerebral anoxia and epilepsy; and
CC   infectious diseases
XX
SQ   Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:   1
Score: 1.6e-59
Percent Similarity: 99.08%   Length: 1336
Best Local Similarity: 99.08%   Matches: 215
Query Match: 99.23%   Conservative: 0
                                       Mismatches: 2
                                       Indels: 0
                                       Gaps: 0

US-09-976-740-7 (1-217) x AAF21860 (1-1336)

```
Qy     1 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    73 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAGATGATGAAGAGATGAGAA 132

Qy    21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133 GATGATGTGTCAGGAGGGCCTCGAAGTCCCCGAGAGTGACCGTCCTCAGGTGCCCAGCAC 192

Qy    41 HisGlnLeuAsnGlyGluArgGlyTyrProGlnSerAlaLysGluGluTrpThr 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   193 CACCAGCTTAACCGACGGGGAGACCCTCAGAGTGCTAAGGAGGTCAAGGAGGTGACC 252

Qy    61 ProCysGlyProHisGlnGlyTyrAspGluGlyArgGlyTyrProAlaProGlySerGlyThr 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 CCCTGCGGACCGCACCAGGGCTACGACGAGGGCCGGGGCTACCCCGCCCCGGGCAGCGGCACC 312

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAAGAAGGGGGAACAGCTTCTGTGGCCACC 372

Qy   101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 GGGCCAGACTCCCCCTCGCCCGTGCCTTTGCCCCCAGGGAAACCAGCCCTACCTGGGGCC 432

Qy   121 AspGlyThrProPheGlyCysProProGlyAlaArgLysGlySerAspSerAspProValGlu 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 GACGGGACCCCCTTTGGCTGTCCCCCCGGGGCGCAAAGAGGAAGCCATCTGATCCGGTCGAG 492

Qy   141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPhePheProGlnGlnAlaThr 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA 552

Qy   161 AlaPheGlnGlnGlnGlnIleAspSerLeuLeuLeuMetGlnArgThrAspVal 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GCTTTCCAAGAGCAGGAAAATTGATGGTCGTCAGCCACCAGAGTGTG 612

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 CTCACCGGGCCTGTCCATCCGCCCTTGAAAATCTACGAGCACCACATCAAG 672

Qy   201 ValLeuGlnLnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   673 GTGCTTCAGCAAGGCCACTTTGAGGATGACCCGATGGCTTCTTAGGC 723
```

RESULT 5
AAH26489

ID   AAH26489 standard; cDNA; 1362 BP.
XX
AC   AAH26489;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag= a
FT   /partial
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PS   Example 2; Fig 12; 143pp; English.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82799.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82799) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at risk for atherosclerosis, methods for evaluating an agent for use
CC   in treating atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 7.15e-53   Length: 1362
Score: 1047.50   Matches: 195
Percent Similarity: 95.45%   Conservative: 15
Best Local Similarity: 88.64%   Mismatches: 7
Query Match: 89.53%   Indels: 3
DB: 5   Gaps: 2

US-09-976-740-7 (1-217) x AAH26489 (1-1362)

Qy   1 GluGluArgValLeuGlyLeuGlyLeuGluGluAspAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||||||||||::|||||||||
Db 37 GAGGAGCGAGTGCTTGGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGACGACGAGGACGAC 96

Qy 21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38

Db 97 GACGACGACGTCGTGTCCGAGGGCTCGGAGGGTGCCCGGAGGACGCGATCGTCCGCGGGTGCG 156
         ||||||...
Qy 39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
         ||||||||||||||| |:||||||||||||||||||||||||||||
Db 157 CAGCATCACCAGCTCAATGACGGGGCGCAGGGCCCCCAGAGCGCCAAGGAGCGCGGCCAAG 216

Qy 58 GluTrpThrProCysGlyProHisGlnAspGlyGlnAsnProGlyGlnAsnProGlyAlaProGly 77
         |||||||||||||||:::
Db 217 GAGTGGTCGCCGTGTGGTCCCCCACCCTGGCCAGGAGAAGGACGCGGGGGCCCCGGGC 276

Qy 78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGluGlyGlyThrAlaSer 97
         ||||||||||||||||||||||||::||||||||||||
Db 277 AGTGGCACCCGCCCAGGTGTTCTCATGGCCGCGATGAACAAGGAGGAGGGGGGGACCGCCTCT 336

Qy 98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
         |||||||||||||||||||||||||||||
Db 337 TCGACACCCGGCCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCGGGGAAGCCAGCCCTC 396

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyValArgLysGlyLysProSerAsp 137
         |||||||||||||||||||||||::||||||||
Db 397 CCAGGAGCCGACGGGACACCCCTTTGGCTGCCCGCCGGGCGTGCGCAAGAGGAAGCCCGGCGAGAC 456

Qy 138 ProValGluTrpThrValMetAspValValGlyTyrPheThrArgLeuAlaGlyPheProGlu 157
         |||||||||||||||||||||||:::|||||||||
Db 457 CCCGTGGAGTGGACAGTGATGGACGTGGTGGGGTACTTCACCCGAGGCGGGGCTTCCCTGAG 516

Qy 158 GlnAlaThrAlaPheGlnGlnLeuGluAspGlyLysSerLeuLeuMetGlnArg 177
         ||||||||||||:::|||||||
Db 517 CAAGCCACGGCTTTCCAGGAGCCAGGAGTCGAACGGGCAAGTCCCTGCTCATGCAGCGC 576

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
         |||||||||||||||||||||||||
Db 577 ACCGGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCAGCGGTTGAAAATCTATGAGCAC 636

Qy 198 HisIleLeuLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
         ||||||||||||||||:::||||||||
Db 637 CATATCAAGGTGCTCGAGCAGGGTCACTTCGAGACGACGATGACCCCAGGAAGGCTTCCTGGGA 696

RESULT 6
AAH26490
ID   AAH26490 standard; cDNA; 1422 BP.
XX
AC   AAH26490;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.
XX
KW   Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag= a
FT   /partial
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX

DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82800.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 13; 143pp; English.
XX
SQ   Sequence 1422 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;

CC   The present sequence is that of cDNA encoding a portion (see AAB82800) of
CC   novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bind to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in
CC   AAH26491. The invention provides claimed polynucleotides encoding novel
CC   polypeptides which are capable of binding to native and methylated LDL,
CC   the isolated polypeptides, termed LBPs, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Also claimed are methods of determining if an
CC   animal is at risk for atherosclerosis, and methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed

Alignment Scores:
Pred. No.:   1
Score: 7.45e-53   1047.50   Length: 1422
Percent Similarity: 95.45%   Matches: 195
Percent Identity: 88.64%   Conservative: 15
Best Local Similarity: 89.53%   Mismatches: 7
Query Match: 5   Indels: 3
DB: Gaps: 2

US-09-976-740-7 (1-217) x AAH26490 (1-1422)

Qy   1 GluGluArgValLeuGlyLysGlyGluGluGluAspAspAspGluAspGluGlu 20
        |||||||||||||||||||||||||||||||:::|||||:::|||||||||||
Db   97 GAGGAGCGGGAGTGCTTGAAAAGAGGAGGAGGAGGAGGAGGACGAGGAGGAC 156

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerArgProAlaGlyAla 38
        |||||| |||||||||||||||||||||||:::||||||||:::|||
Db 157 GACGACGACGTTCGGTCGGAGGGATCCGAGGTGCCGGAGTCCCGGCGGGGTGG 216

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
        |||||||||||||||::: ||||||||||||:::||||||||||:::|||
Db 217 CAGCATCACCAGCTGAATGGCGGCGAGCGCGGGCCGCAGAGCGCGGGCCAAG 276

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluArgGlyProAlaProGly 77
        ||||||||||||::::||||||||:::|||||||||||||||||||:::||
Db 277 GAGTGGTCGCCGTGTGGGCCCCACCCTGGCCAGGACGAGAGGGGCCCGGCGGGC 336

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
        ||||||||||||||||||||||:::|||||||||||||||||||:::|||
Db 337 AGTGGCACCCGCCAGGTGTTCTCCATGGCCGCCATGAACAAGGAATCAGCCTCT 396

Qy   98 ValAlaThrGlyProAspSerProValProLeuProGlyLysProAlaLeu 117
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 397 TCGACCACCGGGCCTGACTCCCCGGTCCCTTGGCCTGCGGGCAAGCCCTC 456

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgGlyLysProSerArgAsp 137
        |||||||||||||||||||||:::|||||||||||||||||||:::|||
Db 457 CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTCCCGGCAGAGAGCCGGCAGAC 516

Qy 138 ProValGlnTrpThrValMetAspValValGluTyrPheThrGlyPheProGlu 157
        ||||||||||||||||||||||||||||||||||||||||||||||:::
Db 517 CCGGTGCAGTGGACAGTCATGGACGTTGTTGAGTACTTCACCGGAGGGCCTGAG 576

Qy 158 GlnAlaThrAlaPheGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
        |||||||||||||||||||||||||:::||||||||||||||||||:::
Db 577 CAAGCCACGGCCTTCCAGGAGCAGGAGGATCGGGAAGTCCCTGCTCACGCAGCGGC 636

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
        |||:::||||||||||||||||||||||||||||||||||||||||||
Db 637 ACCGGATGTCCTCACCGGCGCCTTGTCCATCCGCCTGTGGGGCCCAGCGCTTGAAAAAT 696

Qy 198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAlaAspAspProAspGlyPheLeuGly 217
        ||||||||||||||||||||:::|||||||||||||||||||:::|||
Db 697 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGACGGCTTCCTGGGA 756

RESULT 7

AAH26488
ID   AAH26488 standard; cDNA; 1617 BP.
XX
AC   AAH26488;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   1..955
FT   /*tag= a
FT   /partial
FT   /note= "includes in-frame stop codon at nucleotides
FT   28..30"
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82798.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 11; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82798) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bind to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at risk for atherosclerosis, and methods for evaluating an agent for use
CC   in treating atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1617 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1
Score: 8.44e-53   1047.50   Length: 1617
Percent Similarity: 95.45%   Matches: 195
                                         Conservative: 15

Best Local Similarity: 88.64%　　　Mismatches: 7
Query Match: 89.53%　　　Indels: 3
DB:　　　Gaps: 2

US-09-976-740-7 (1-217) x AAH26488 (1-1617)

```
Qy    1 GluGluArgValLeuGlyLysGlyGluGlyLeuGlyLeuAspAspAspGluAspGluGlu   20
        |||||||||||||||||||||||||||||||||::::::::::
Db  292 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGACGAGGACGAC          351

Qy   21 AspAsp------ValSerGlyGlySerGluValProGluSerAspArgProAlaGlyAla   38
        ||||||      |||||||||||||||||||||||||||||||||||||||||
Db  352 GACGACGACGGTCGTGTCCGGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCGGCGGGTGG 411

Qy   39 GlnHisHisGlnLeuAsn------GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
        |||||||||||||||         |||||||||::::|||||||||||
Db  412 CAGCATCACCAGCTGAAATGGCGGCGGAGCGCGGCCCGCAGAGCGCGAAGGAGCGGGGCCAAG 471

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly   77
        |||||||||::::|||||||||||||||:::|||||||||||
Db  472 GAGTGGCGTCGTGTGGGCCCCCACTGGAGGAAGGGGGCCGCGGGCCCGGGGGC         531

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
        |||||||||||||||||||||||||||||::::|||||||||||||
Db  532 AGTGGCACCCCCCAGGTGTTCTCCATGGCGGCGGCGATGAATAAGGAGGGGGATCAGCCCTCT 591

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyGlyLysProAlaLeu 117
        |||||||||||||||||||||::::|||||||||||||||||
Db  592 TCGACCACCGGGCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTC     651

Qy  118 ProGlyAlaAspGlyThrProProGlyCysProProGlyAlaArgLysGlyLysProSerSerAsp 137
        ||||||||||||||||||||::::|||||||||||||||||::||
Db  652 CCAGGAGCCGATGGGACCCCCTTTGGCTGTCCTCCTGGCGTGCCCGGAAAGAGAAGCCCGACGAC 711

Qy  138 ProValGlyTrpThrValMetAspValValGlyTyrPheThrGluAlaGlyPheProGly     157
        |||||||||||||||||||||||||||||||||||||||||||||
Db  712 CCCGTGGAGTGGACAGTCATGGACGTCGTGGGATACTTCACGGAGGCGGGCTTCCCTGAG      771

Qy  158 GlnAlaThrAlaPheGlnLeuGlnIleAspGlyTyrLysSerLeuLeuLeuMetGlnArg     177
        ||||||||||||||||||||:::|||||||||||||||||||||||||
Db  772 CAAGCCACGGCTTTCCAGGACGCAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC       831

Qy  178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis    197
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  832 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCGGCACTGAAAATCTATGAGCAC    891

Qy  198 HisIleLysValLeuGlnHisGlnHisPheGluAspAspAspProAspGlyPheLeuGly    217
        |||||||||||||||||||||||:::||||||||||||||||
Db  892 CATATCAAGGTGCTGCAGCACCAGCACTTCGAGGACGACGACCCGGACGGCTTCCTGGGA   951
```

RESULT 8

```
ID   AAH26500 standard; cDNA; 2561 BP.
XX
AC   AAH26500;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key            Location/Qualifiers
FT   CDS            246..1928
FT                  /*tag= a
XX
PN   WO20016874-A2.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-05217849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM,  Lees RS,  Law SW,  Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82807.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Claim 4; Fig 2A; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding novel rabbit low density
CC   lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was
CC   isolated following screening of a rabbit cDNA library for clones encoding
CC   LBPs that bound to both native low density lipoprotein (LDL) and methyl
CC   LDL. The invention provides claimed polynucleotides encoding novel
CC   polypeptides which are capable of binding to native and methylated LDL,
CC   the isolated polypeptides, termed LBPs, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Also claimed are methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;
XX
```

Alignment Scores:
Pred. No.:
Score: 1.32e-52
Percent Similarity: 1047.50
Best Local Similarity: 95.45%
Query Match: 88.64%
                           89.53%

Length: 2561
Matches: 195
Conservative: 15
Mismatches: 7
Indels: 3
Gaps: 2

US-09-976-740-7 (1-217) x AAH26500 (1-2561)

```
Qy    1 GluGluArgValLeuGlyLysGlyGluGlyLeuGlyLeuAspAspAspGluAspGluGlu   20
        |||||||||||||||||||||||||||||||||::::::::::
Db 1296 GACGAGCGAGTGCTTCCGGAGGGCTCGGAGGTGCCCGAGAGCCGATCGTCCCGGCGGGTGG 1355

Qy   21 AspAsp------ValSerGlyGlySerGluValProGluSerAspArgProAlaGlyAla   38
        ||||||      ||||||||||||||||||||||||||||||||||
Db 1236 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGACGAGGACGAGGACGAC    1295

Qy   39 GlnHisHisGlnLeuAsn------GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
        |||||||||||||||         |||||||||::::|||||||||
Db 1356 CAGCATCACCAGCTGAAATGGCGGCGGAGCGCGGCCCGCAGAGCGCGAAGGAGCGGGGCCAAG 1415

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly   77
        |||||||::::||||||||||||||||:::|||||||||||
Db 1416 GAGTGGCGTCGTGTGGGCCCCCACTGGAGGAAGGGGGCCGCGGGCCCGGGGC          1475

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
        |||||||||||||||||||::::|||||||||||
Db 1476 AGTGGCACCCCGCCAGGTGTTCTCCATGGCGGCGGCGATGAATAAGGAGGGGGGATCAGCCCTCT 1535

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyGlyLysProAlaLeu 117
        ||||||||||||||||||||::::||||||||||||||||
Db 1536 TCGACCACCGGGCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTC     1595

Qy  118 ProGlyAlaAspGlyThrProProGlyCysProProGlyAlaArgLysGlyLysProSerSerAsp 137
        |||||||||||||||||||||::::|||||||||||||||||||||||::||
Db 1596 CCAGGAGCCGATGGGACCCCCTTTGGCTGTCCTCCTGGCGTGCCCGGAAAGAGAAGCCCGAC 1655
```

CC This cDNA clone codes for novel rabbit low density lipoprotein (LDL)
CC binding protein LBP-2 (see AAW49038). It was isolated by functional
CC screening of a cDNA library, produced from balloon-deendothelialised
CC healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to
CC bind both native and methyl LDL. cDNA clones (see AAV32834-33) and
CC encoded rabbit and human LBPs (see AAW49037-42) are claimed. An
CC abnormality in an aspect of LBP metabolism or structure is diagnostic of
CC a risk for atherosclerosis. The invention provides: methods for
CC determining if an animal is at risk for atherosclerosis (e.g. for
CC prenatal screening); methods for treating atherosclerosis (including gene
CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC formation of atherosclerotic plaque; and methods for treating a cell
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC vaccine compositions are also provided, as well as recombinant vectors
CC and host cells used to produce recombinant LBP

SQ Sequence 1617 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

US-09-976-740-7 (1-217) x AAV32835 (1-1617)

Alignment Scores:
Pred. No.:
Score: 1.89e-52   Length: 1617
                        1041.50   Matches: 194
Percent Similarity: 95.00%   Conservative: 15
Best Local Similarity: Mismatches: 8
  Percent Similarity: 88.18%   Indels: 3
  Query Match: 89.02%   Gaps: 2
DB: 2

Qy   1 GluGluArgValLeuGlyLysGluGluGluIleAspGlyLysSerAspGlnGluProGlyProGly 20
        ||| ||| ||||||| ||| ||||||| ||| |||||||| ||: |:|||||||:||||:|||
Db 292 GAGGAGCGCAGTGCTTGAAAAGAGGAGGAGGAGGAGGAGGAAGACGACGAGGAGGAGAC 351

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspAspArgProAlaGlyAla 38
        |||||| |||||:|||||||||:|||||:|||:||:|||||||||||||:||:||||
Db 352 GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGACGACCGTCCCGGCGGGTGCG 411

Qy   39 GlnHisHisGlnIleLeuAsn---GlyLeuArgGlyProGlnSerAlaLysGluArgValLys 57
        ||| ||||||||:|||||||| |||||:|||||||||||||||||||||:||||||:|||
Db 412 CAGCCATCACCAGCTGAATGGGCGGCGGCGGCGGCGGCAGCCGCCCAAGGAGACGCGGCCAAG 471

Qy   58 GluTrpThrProCysGlyProHisGlnGlyLeuGlnGlyAspGlyArgGlyProAlaProGly 77
        ||||||||||||||||||||:|||||||||:||||||||||||||||||||||||||||||
Db 472 GAGTGGACCCCGTGCTGGTGTGGSCCCCACCCCTGGGCCAGGAGGAGGAAGGGGGGGGGGGC 531

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
        |||||||||||||||||||:||:||||||||||:|:|||:||||||:||:|||||||||
Db 532 AGTGGCACCCGCCGCCAGGTGTTCTCCATGGCGGCGGCCTTGAGTAAGGAGGGGGGARCAGCTCT 591

Qy   98 ValAlaThrGlyLeuProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
        |||||||||||||||||||||||||||||:||||||||||||:|||||||||||||||||||
Db 592 TCGACCACCGGCCTGACTCCCGGCGTCCCGGTCCTTTTGCCCCCTGGGAAGCCAGCCCTC 651

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysSerProSerAsp 137
        |||||||||||||||||||||||:|||:||||||:|||:|||||||||:||||||:|||:||:
Db 652 CCAGGAGGCCGATGGGACCCCCTTTTGGCTGCCCGGGCGGAAGGAGAAGAGCCCGAGCGAGAC 711

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPhePheProGlu 157
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 712 CCCGTGGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGGAGGCGGGCGGCTTCCCTGAG 771

Qy 158 GlnAlaThrAlaPheGlnGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 772 CAAGCCACGGCCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC 831

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 832 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCTGCGGTTGAAAATCTATGAGCAC 891

RESULT 9
AAV32835
ID   AAV32835 standard; cDNA; 1617 BP.
XX
AC   AAV32835;
XX
DT   09-NOV-1998 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW   receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Oryctolagus cuniculus.
XX

FH   Key   Location/Qualifiers
FT   CDS   1..954
FT   misc_feature   156..1617
FT   /*tag= a
FT   misc_feature   156..954
FT   /*tag= b
FT   /note="Claim 5"
FT   misc_feature   196..1617
FT   /*tag= c
FT   /note="Claim 6"
FT   misc_feature   313..396
FT   /*tag= d
FT   /note="Claim 18"
FT   misc_feature   313..360
FT   /*tag= e
FT   /note="Claim 19"
FT   misc_feature   361..396
FT   /*tag= g
FT   /note="Claim 20"
FT   misc_feature   631..660
FT   /*tag= h
FT   /note="Claim 21"

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPhePheProGlu 157
Db 1656 CCCGTGGGAGTGGGACAGTCATGGACGTGGAGTACTTCACCGGAGGCGGGCGGCTTCCCTGAG 1715

Qy 158 GlnAlaThrAlaPheGlnGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 1716 CAAGCCACGGCCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC 1775

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 1776 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCTGCGGTTGAAAATCTATGAGCAC 1835

Qy 198 HisIleLysValLeuGlnGlnGlyHisPheGlyLeuAspAspAspSerProAspGlyPheLeuGly 217
Db 1836 CATATCAAGGTGCTTCAGCAGGGTCACTTCGGACGATGACCCGGACGGATTCCTGGGA 1895

PA   (BOST-) BOSTON HEART FOUND INC.
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and

```
Qy      198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
            ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db      892 CATATCAAGGTGCTGCAGCAAGGTCACTTCGAGGACGATGACCCGGAAGGCTTTCCTGGGA 951

CC          expression vectors, cells and methods of producing the LBPs. Methods of
CC          determining if an animal is at risk for atherosclerosis, methods for
CC          evaluating an agent for use in treating atherosclerosis, and methods for
CC          treating a cell having an abnormality in structure or metabolism of LBP
CC          are claimed. Pharmaceutical compositions comprising an LBP polypeptide or
CC          nucleic acid, and vaccine compositions, are also claimed
XX
SQ          Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

RESULT 10
AAH26495
ID      AAH26495 standard; DNA; 12425 BP.
XX
AC      AAH26495;
XX
DT      12-NOV-2001 (first entry)
XX
DE      Human low density lipoprotein binding protein 2 (LBP-2) gene.
XX
KW      Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW      atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW      ds.
XX
OS      Homo sapiens.
XX
FH      Key             Location/Qualifiers
FT
FT      CDS             2832..5153
FT                      /*tag= a
FT                      /note= "includes introns"
FT      exon            2832..3785
FT                      /*tag= b
FT      intron          3786..4207
FT                      /*tag= c
FT      exon            4208..4502
FT                      /*tag= d
FT      intron          4503..4593
FT                      /*tag= e
FT      exon            4594..4694
FT                      /*tag= f
FT      intron          4695..4787
FT                      /*tag= g
FT      exon            4788..4899
FT                      /*tag= h
FT      intron          4900..4994
FT                      /*tag= i
FT      exon            4995..5153
FT                      /*tag= j

Alignment Scores:
Pred. No.:
Score:                  2.68e-51        Length:          12425
Percent Similarity:     1036.50         Matches:         216
Best Local Similarity:  69.01%          Conservative:    0
Query Match:            69.01%          Mismatches:      1
DB:                     88.59%          Indels:          97
                        5               Gaps:            3

US-09-976-740-7 (1-217) x AAH26495 (1-12425)

PN      WO20016874-A2.
PD      07-SEP-2001.
XX
Qy        1 GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluGluAspGluGlu 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4217 GAAGAGCGAGTACTTGAAGAAGAAGAAGAAGAAGATGATGATGAAGATGAAGAA 4276

PA      (BOST-) BOSTON HEART FOUND INC.
XX
Qy       21 AspAspValSerGluGlyValProGluSerAspArgProAlaGlyAlaGlnHis 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4277 GATGATGTGTCAGAGGGCGTCTCAGAAGTGCCCGAGAGTGACCGTCCTGCAGCAC 4336

PI      Lees AM,  Lees RS,  Law SW,  Arjona AA;
XX
Qy       41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4337 CACCAGCTTAACGGCGAGCGGGGCCCCCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 4396

PR      14-JUL-2000; 2000US-0061628289.
PR      02-MAR-2000; 2000US-0051784849.
XX
Qy       61 ProCysGlyProHisGlnGlyTyrGlnAspGlyIleArgGlyProAlaProGlySerGlyThr 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4397 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGGCCAGCCCCGGCAGGGCACC 4456

PT      28-FEB-2001, 2001WO-US006356.
XX
Qy       81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyTyr--------- 95
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     4457 CGCCAGGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGATACCCTCT 4516

PT      diagnosing and/or identifying therapeutic agents for atherosclerosis.
PF      New isolated low density lipoprotein binding polypeptide for treating,
XX
Qy       95 ---------------------- 95
            ||||||||||||||||||||||
Db     4517 GGGGTGGGGGGAAGAGTTGCTAGGTGGAGGAGAAACTCAGCCCCGAAGACAAAAGCCAAAGACAGGT 4576

DR      P-PSDB; AAB82806.
DR      WPI; 2001-565505/63.
XX
Qy       96 -----------AlaSerValAlaThrGlyProAspSerProSerProValProIle 110
                       ||||||||||||||||||||||||||||||||||||||||
Db     4577 GTTTTTTTTCCTTCCCAGCTTCCGTTGCCACCGGCGCCCCAGACTCCCCGTCCCCGGCCTTT 4636

Qy      110 uProProGlyLysProAlaLeuProGlyValAlaAspGlyIleArgTyrProPheGlyCysPro----- 128
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4637 GCCCCCCAGGCCAAACCAGCCCTACCTGGGGGCCGACGCGGACCCCCTTTTGGCTGTCCGTAAGT 4696

Qy      128 -------------------------------------------- 128
            
Db     4697 TGGGGTATTGGAGACATGGGGGTGTCTCAGGTGTGTGTACAGCCAGAGACATCCG 4756

Qy      129 ------------------------------------------------ 129
            
Db     4757 TGTTCACTCGGTGTCGTGGTTGTTTGTTTGTTTGATCGCAGTCCCGGCGCCGCAAAGAGAAGCCATCTGATC 4816

Qy      138 roValGluTrpThrValMetAspValValGluTyrProPheThrGluAlaGlyLysPheProGluGluG 158
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4817 CCGTTCGAGTTGGACCGTGATGGAGTTCGTTCGGAATATATTTTACTGAGGCCTGGAATTCCCGGAGC 4876

PS      Example 4; Fig 23; 143pp; English.
XX
Qy      158 lnAlaThrAlaPheGlnGlu---------------------------------------------- 164
            |||||||||||||||||
Db     4877 AGGGCACAGCGTTTCCAAGA--GCAGTGAGTTTCCAGCCCCAGGACTACACACTGACAGACA 4935

Qy      165 -------------------------------------------------------GlnG 166
                                                                   |||
Db     4936 CAGAGGGCCTCCCTGGGGATGTGCCCGATCCCGGCTTTCTCGTTCTCGTTCCCACCCAGG 4995

Qy      166 luIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerI 186
            ||||||
Db            
```

```
Db   4996 AAATTGATGGAAATCTTTGCTGCTCATGCAGCAGCCACAGATGTGTGCTCACCGGCCCTGTCCA 5055
Qy    186 leArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGlyH 206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5056 TCCGGCCTCGGGCCCAGCCCTGAAAATCTACGAGCACCATCAAGGTGCTTCAGCAAGGCC 5115
Qy    206 isPheGluAspAspProAspGlyPheLeuGly 217
          |||||||||||||||||||||||||||
Db   5116 ACTTTGAGGATGAATGACCCGGATGGCTTCTTAGGC 5150
```

RESULT 11

ID   AAC59574 standard; cDNA; 1134 BP.
XX
AC   AAC59574;
XX
DT   26-JAN-2001 (first entry)
XX
DE   Human secreted protein gene 9 SEQ ID NO:19.
XX
KW   Human; secreted protein; diagnosis; neuroprotective; cytostatic;
KW   cardioactive; immunomodulatory; muscular active general; vulnerary;
KW   gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW   and antibacterial; gene therapy; detection; cancer; chromosome marker;
KW   chromosome identification; neural disorder; immune disorder;
KW   muscular disorder; reproductive disorder; gastrointestinal disorder;
KW   pulmonary disorder; cardiovascular disorder; renal disorder;
KW   proliferative disorder; wound healing; infectious disease; preservative;
KW   food additive; ss.
XX
OS   Homo sapiens.
XX
PN   WO200005683-A1.
XX
PD   28-SEP-2000.
XX
PF   16-MAR-2000; 2000WO-US006822.
XX
PR   23-MAR-1999; 99US-0126054P.
PR   10-DEC-1999; 99US-0169916P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM, Komatsoulis G;
XX
DR   WPI; 2000-587666/55.
DR   P-PSDB; AAB34307.
XX
PT   Human secreted proteins and gene sequences encoding them, useful for
PT   detecting, preventing, and treating disorders such as cancer,
PT   neurological disorders and immune system disorders.
XX
PS   Claim 1; Page 344; 429pp; English.
XX
CC   The polynucleotide sequences given in AAC59566 to AAC59614 encode the
CC   human secreted proteins given in AAB34299 to AAB34347. AAB34348 to
CC   AAB34437 represent human secreted polypeptide sequences and proteins
CC   homologous to them, which are given in the exemplification of the present
CC   invention. Human secreted proteins have activities based on the tissues
CC   and cells the genes are expressed in. Example of activities include:
CC   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular
CC   active general; vulnerary; gastrointestinal; nephrotropic; antiinfective;
CC   gynaecological; and antibacterial. The polynucleotides can be used for
CC   the detection of various disorders such as cancer, chromosome other
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The secreted proteins can be used to treat
CC   disorders such as neural, immune muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wound healing, and infectious diseases. The proteins can also
CC   be used as a food additive or preservative to increase or decrease
CC   storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
CC   sequences used in the exemplification of the present invention
XX

SQ   Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:
Score: 4.14e-39   Length: 1134
                        811.00   Matches: 151
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 99.34%   Mismatches: 1
Query Match: 69.32%   Indels: 0
DB: 3   Gaps: 0

US-09-976-740-7 (1-217) x AAC59574 (1-1134)

```
Qy   66 GlnGlyGlnAspGluGlyAlaGlyGlyProAlaProGlySerGlyThrArgGlnValPheSer 85
        ||||||||||||||||||||||||||||||||||||||||
Db  921 CAGGGGCAGGATGAAGGGCGTGGGGGGCCAGCCCCCGGGGAGCGGCACCCGCCAGGTGTTCTCC 862

Qy   86 MetAlaAlaMetAsnLysGluGlyYGlyThrAlaSerValAlaThrGlyProAspSerPro 105
        |||||||||||||||||||::|||||||||||||||||||||||
Db  861 ATGGCAGCCATGAACAAGGAAGGGGGGGGAACAGCTTCTGTTGCCACCGGGCCAGACTCCCG 802

Qy  106 SerProValProLeuProProGlyLysProAlaLeuAlaProGlyValAlaAspGlyThrProPhe 125
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  801 TCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTCGCCCCTGGGGGTCGCAGACGGGAACCCCTTT 742

Qy  126 GlyCysSerProGlyArgGlyLysGlyLysProSerAspAspProValGluTrpProThrValMetAsp 145
        ||||||||||||||||||||||||||||||||||||||||||||
Db  741 GGCTGTTCCTCCGGGCGCGGCAAAGGAAAGCCATCGGATCCCGTCGAGTGGCCGACGGTGATGGAT 682

Qy  146 ValValGluTyrPheThrArgGluAlaGlyGlnAlaThrAlaPheGlnGluGln 165
        ||||||||||||||||||||||||||||||||||||||
Db  681 GTCGTCGAATATTTTACTGAGGCTGGATTCCCGGACGGGCAGCAGCTTTCCAAGAGCAG 622

Qy  166 GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGlyLeuSer 185
        |||||||||||||||||||||||||||||||||||||
Db  621 GAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGGACAGAGATGTGCTCACCGGCCCTGTCC 562

Qy  186 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGlyHisPheGluGly 205
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  561 ATCCGCCTCGGGCCCAGCCCTGAAAATCTACGAGCACCATCAAGGTGCTTCAGCAAGGCC 502

Qy  206 HisPheGluAspAspProAspGlyPheLeuGly 217
        ||||||||||||||||||||||||||||
Db  501 CACTTTGAGGATGATGACCCGGATGGCTTCTTAGGC 466
```

RESULT 12

ID   ADB49888 standard; DNA; 460 BP.
XX
AC   ADB49888;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:430.
XX
KW   toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW   toxicity marker; toxicity progression; drug screening;
KW   primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO2003065993-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-US003482.
XX
PR   04-FEB-2002; 2002US-0353171P.
PR   13-MAR-2002; 2002US-0363534P.
PR   08-APR-2002; 2002US-0370249P.
PR   10-APR-2002; 2002US-0370248P.
PR   10-APR-2002; 2002US-0371114P.
PR   10-APR-2002; 2002US-0371135P.
PR   10-APR-2002; 2002US-0371109P.
PR   10-APR-2002; 2002US-0371150P.
PR   11-APR-2002; 2002US-0371413P.

```
PR   19-APR-2002;  2002US-0373601P.
PR   19-APR-2002;  2002US-0373602P.
PR   22-APR-2002;  2002US-0374139P.
PR   08-MAY-2002;  2002US-0374370P.
PR   09-MAY-2002;  2002US-0376450P.
PR   09-MAY-2002;  2002US-0378653P.
PR   09-MAY-2002;  2002US-0378655P.
PR   09-JUL-2002;  2002US-0394230P.
PR   09-JUL-2002;  2002US-0394253P.
PR   04-SEP-2002;  2002US-0407688P.
PR   28-JAN-2003;  2003US-0442900P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D,  Porter M,  Johnson K,  Higgs B,  Castle A,  Orr M;
PI   Blashoff M;
XX
DR   WPI; 2003-731472/69.
XX

Claim 44; SEQ ID NO 430; 874pp; English.

CC   The present invention describes a method for determining whether a
CC   compound induces a toxic effect on a tissue or cell. The method comprises
CC   preparing a gene expression profile of a tissue or cell sample exposed to
CC   the compound, and comparing the gene expression profile to a database
CC   comprising data or information on the Tox mean and non-Tox mean value.
CC   The method is useful for predicting or identifying at least one toxic
CC   effect, particularly hepatotoxicity, of a test or unknown compound. The
CC   genes listed in the specification are useful as diagnostic or toxicity
CC   markers for the prediction or identification of the physiological state
CC   of tissue or cell sample that has been exposed to a compound, or to
CC   identify or predict the toxic effects of a compound or an agent. These
CC   may also be used as markers for monitoring toxicity progression or for
CC   drug screening. The present sequence represents a primary rat hepatocyte
CC   toxicity modelling related gene sequence from the present invention.
XX
SQ   Sequence 460 BP; 110 A; 119 C; 126 G; 105 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                       2.01e-18     Length:         460
Percent Similarity:          451.00       Matches:         82
Best Local Similarity:       82.52%       Conservative:     3
Query Match:                 79.61%       Mismatches:      12
                             38.55%       Indels:           6
                             9            Gaps:             1

US-09-976-740-7 (1-217) x ADB49888 (1-460)

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyGlnGlyArgGlyAlaProGly  77
           |||||||||::|||||||||||||||||||||||||||||||||
Db  459 GAGTGGTCGCCCTGTGGACCTTTCCAGGGCCAGGATGAAGGGCGGGGACCAGCACCTGGC 400

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGlnGlyValGlyThrAlaSer  97
           ||||||||||||:::||||||||||||||||||||::::||
Db  399 AGCTGCACACCAGGTGTTTCGATGACAGCTATGAAATAAAGAAGAGGGGGATCGGCTTGT 340

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
           |||||||||||||||||||||||:::|||||||
Db  339 GTTACAGCTGCTCCAGATTCTCCATCTCCTGTGCCTTTGCCTCCAGGAAAACCAGCCCTA 280

Qy  118 ProGlyValAlaAspGlyThrProHisGlyCysProProGlyArgGlyLysGlyLysProSerAsp 137
           |||||||||||:::||||||||||||||:::||
Db  279 CCTGGGGGCTGATGGGACACACCACATTTGGCTGTGCCTCCTGGGCGGCAAGGAGAAGCCAACGGAC 220

Qy  138 ProValGluTrpThrValMetAspValValGluThrTyrPheThrGluLeuGlyPheProGlu 157
           |||||||||||||||||||||||
Db  219 CCAGTGGAGTGGACAGTCATGGATGTGGTGGTT--------------TTTCCTCGT 178
```

```
Qy  158 GlnAlaThr 160
           |||
Db  177 CCCACCACC 169

RESULT 13
ADA53650
ID   ADA53650 standard; cDNA; 1566 BP.
XX
AC   ADA53650;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human coding sequence, SEQ ID 1218.
XX
OS   Homo sapiens.
XX
PN   EP1293569-A2.
XX
PD   19-MAR-2003.
XX
PF   21-MAR-2002; 2002EP-00006586.
XX
PR   24-JAN-2002; 2002US-0350435P.
PR   14-SEP-2001; 2001JP-00328381.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-395539/38.
DR   P-PSDB; ADA55289.
XX
PT   New polynucleotides encoding full-length polypeptides, e.g. secretory
PT   and/or membrane proteins, useful for developing medicines for disease in
PT   which the gene is involved, or as target molecules for gene therapy.
XX
CC   The present invention relates to novel human secretory or membrane
CC   proteins (ADA54072-ADA57710) and their coding sequences (ADA52433-
CC   ADA54071). The coding sequences are useful in the gene therapy of
CC   diseases caused by abnormalities of the proteins, e.g. cancer,
CC   inflammatory diseases, osteoporosis or neurological disease.
XX
PS   Claim 1; SEQ ID NO 1218; 205pp; English.
XX
KW   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW   Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW   inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX
DE   Human coding sequence, SEQ ID 1218.
XX
SQ   Sequence 1566 BP; 428 A; 317 C; 347 G; 474 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                       2.16e-09     Length:        1566
Percent Similarity:          305.50       Matches:         75
Best Local Similarity:       47.72%       Conservative:    19
Query Match:                 38.07%       Mismatches:      54
                             26.11%       Indels:          49
                             7            Gaps:             6

US-09-976-740-7 (1-217) x ADA53650 (1-1566)

Qy   29 ValProGluSerArgArgProAlaGlyAlaGlnHisHisGlnLeu------AsnGlyGlu  46
           :||:||:    |||||:::
Db   46 ATTCCTGGGGGCCCCCCCCTCCGACCCCGCGGCGCGGCTGGACTACAACTCCCGG 105

Qy   47 ArgGlyPro------GlnSerAlaLysGluArgValLysGluTrpThrProCysGlyPro  64
           :::         |||||||
Db  106 CGTGCCGCGCGGCCGTCGGCCGCTGCACCCGGCGGGCTTTGCCGCGTGGCGGCCG------ 156

Qy   65 HisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal--  83
           |||||
Db  219
```

Db 157 -------CCGAGCTCCGCGCGGGGGGGGCGGCGGGCCATGCGGGGGAGTTGCT 207

Qy 84 -----------PheSerMetAlaAlaMetAsnLysGluGly 93
                 |||::: |||||||
Db 208 GAAGTAAAGGAAACCTGCAGCCTTCCCATGCTATCTGTTGACATGGAAAACAAGGAAAT 267

Db 94 GlyThrAlaSerValAlaThrGlyProAspSerProSerProValProLeuProProGly 113
             ::: |||:::
Db 268 GGCTCTGTCGCGTGTAAAAAATTCCATGGAAAAT------- 300

Qy 114 LysProAlaLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlu 133

Db 301 -------------------GGGAGA------ 306

Qy 134 LysProSerAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAla 153
            :::|| |||||||||||||
Db 307 ---CCACCTGATCCTGCAGACTGGACAGGACTTCAGTTAAAATTGGGGGCCTGCTCTGAAA 363

Qy 154 GlyPheProGlyGlnAlaThrAlaPheGlnGluGlnGlnIleLeuAspGlyLysSerLeuLeu 173
            |||:::||||||::::|||||
Db 364 GGATTGAGGAGGAGCAAGCTACTGCTTTTCAGGAACAGGAAAAATCCCGTGCTA 423

RESULT 14

ABA91317

ID   ABA91317 standard; DNA; 1957 BP.
XX
AC   ABA91317;
XX
DT   08-APR-2002 (first entry)
XX
DE   Human colon specific gene 407124.
XX
KW   Colon specific gene; CSG; gene; human; colon cancer; tumour; metastasis;
KW   diagnosis; gene therapy; imaging; staging; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO20019528-A2.
XX
PD   06-DEC-2001.
XX
DT   29-MAY-2001; 2001WO-US017583.
PR   26-MAY-2000; 2000US-0207383P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Macina RA, Chen S, Pluta J, Sun Y, Recipon H;
XX
DR   WPI; 2002-083188/11.
XX
PT   Colon specific polypeptides and polynucleotides useful for diagnosing,
PT   monitoring, staging and treating colon cancer.
XX
PS   Claim 1; Page 110-111; 116pp; English.
XX
CC   The present sequence is that of a colon specific gene (CSG), designated
CC   LSGold gene 407124. This is 1 of 22 claimed CSGs (see ABA91303-23)
CC   identified in the Incyte LIFESEQ Gold database using the data mining
CC   Cancer Leads Automatic Search Package (CLASP), which identifies highly
CC   expressed organ and cancer specific genes. The CSG, or its encoded
CC   protein, can be used as a diagnostic marker of colon cancer. The
CC   invention provides claimed methods of diagnosing colon cancer, diagnosing
CC   metastasis of colon cancer, staging colon cancer, monitoring colon cancer
CC   for the onset of metastasis, and monitoring a change in stage of colon

CC   cancer in a patient, by determining the level of a CSG in a sample of
CC   cells, tissues or body fluid and comparing it with the level in a
CC   corresponding sample from a healthy human control or from a sample taken
CC   previously from the patient. Also claimed are methods of identifying
CC   therapeutic agents for use in imaging and treating colon cancer.
CC   Treatment may involve administering a compound which downregulates
CC   expression or activity of a CSG. Adoptive immunotherapy and gene therapy
CC   methods may be used. A claimed vaccine for treating colon cancer
CC   comprises a claimed CSG
XX
SQ   Sequence 1957 BP; 510 A; 449 C; 457 G; 541 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 300.00
Percent Similarity: 50.48%
Best Local Similarity: 38.94%
Query Match: 25.64%
DB:

Length: 1957
Matches: 81
Conservative: 24
Mismatches: 62
Indels: 41
Gaps: 8

US-09-976-740-7 (1-217) x ABA91317 (1-1957)

Qy 25 GluGlySerGluValProGluSer----------AspAlaProAla-----------GlyAlaGlnHis 40
           ||| ::: |||||||
Db 349 GAGAACGCCACACCTCCACCCTCCACTTTCCAAAGAACGCGGGTTCCCCGGGGAGCCCCAC 408

Qy 76 -------------------ProGlySerGlyThrArgGlnValPheSerMetAlaAlaMe 89
                                   ::
Db 467 ----TGTGCCACGTGCCACAGAGAGTCGTGTGGCCTCCGGCCCGGCGGGCTGCTCGGTCCAAGA 522

Qy 41 HisGlnLeuAsnGlyGluArgGlyLysPro--GlnSerAlaSerValAlaThrGlyProAspSe 60
           ::: ||| ||| :::
Db 409 ACTAAACCCAGGGAACTGCCTCTCCGGTGAAAAGTCTTAGCCAGAAACTTTCCCGCGCTT-- 466

Qy 89 tAsnLys-------------GluGlyGlyThrAlaSerValAlaThrGlyProAspSe 104
            :::
Db 583 GAGACGCCATTCCCGGCGTCCGGTGAAAAGGCACTATATCCATC------------- 625

Qy 104 rProSerProValPro---LeuProProGlyLysProAlaLeuProGlyAlaAspGlyTh 123
            |||::: ||| :::
Db 626 ----CCTGCATCGTCTCCAAGACTCAATTCCCTCTAAACCTTCAAGTTCCATGGAAAATGGG-- 682

Qy 123 rProPheGlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThrVa 143
                                                           :::
Db 683 --------------AGACCACCTGATCCTGCAGACTGGGGCGT 711

Qy 143 lMetAspValValGluTyrPheThrGluAlaGlyPheProGlyGlnAlaThrAlaPheGl 163
            ||||||||||| ||| |||||||||||||
Db 712 GATGGATGTCGTCAATTATTTCCGAACCGTGGGATTTGAGGAGCAAGCTAGTGCTTTTCA 771

Qy 163 nGluGlnGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGl 183
            |||:::||||| :::|||||
Db 772 GGAACAGGAAAAATTGGATGGAAAAATCCCTGCTATTGACACAGAAAATGATGGTTGACAGG 831

Qy 183 yLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGl 203
            |||:::||||| :::|||||::::|||||||
Db 832 ACTTCAGTTAAAATTGGGGCCTGCTCTGAAAATCACGAAAATCACGTAAAACCTCTGCA 891

Qy 203 nGlnGlyHisPheGluAspAsp 210
            ||||::::|||||
Db 892 GACAAAGCATTTAAAGAACAAC 913

Qy 174 LeuMetGlnArgThrArgAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLys 193
            |:::||| :::|||||||||::::||||||||:::
Db 424 TTGATGACAAGAGAAATGAGTGGTTGACAGGACTTCAGTTAAAATTGGGGGCCTGCTCTGAAA 483

Qy 194 IleTyrGluHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAsp 210
            |||::::||||||||::::|||||
Db 484 ATCTACGAATATCATGTAAAACCCTGCGAGACAAAGCATTTAAAGAACAAC 534

RESULT 15

AAS75500/c

ID   AAS75500 standard; cDNA; 483 BP.
XX
AC   AAS75500;
XX
DT   13-FEB-2002 (first entry)

```
XX
DE   DNA encoding novel human diagnostic protein #11304.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; AEG11313.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 11304; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences.(I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (III). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement.(II) and its binding partners are useful in medical imaging
CC   of sites expressing (III). (I) and (III) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention.Note:The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 483 BP; 127 A; 112 C; 87 G; 157 T; 0 U; 0 Other;

US-09-976-740-7 (1-217) x AAS75500 (1-483)

Alignment Scores:
Pred. No.:                  1.09e-08
Score:                      285.00          Length:          483
Percent Similarity:         57.81%          Matches:         60
Best Local Similarity:      46.88%          Conservative:    14
Query Match:                24.36%          Mismatches:      26
DB:                         5               Indels:          28
                                            Gaps:            2


Qy     83 ValPheSerMetAlaAlaMetAsnLysGlyGlyThrAlaSerValAlaThrGlyPro 102
          ::                        ||||||:||       ||||:||
Db    396 ATGCTATCTGTTGACATGGAAAACAAAGGAAAAATGGCTCGTCGGTGTAAAAATTCCATG 337

Qy    103 AspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGly 122
          :::::::                        :::::::
Db    336 GAAAAT-------------------------------------------------- 331
```

```
Search completed: March 12, 2004, 21:08:21
Job time :357.96 secs
```

```
Qy    123 ThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThr 142
          :||                             ::||||
Db    330 -------------------------GGGGAGA------CCACCTGATCCTGCGAGACTGGGGC 301

Qy    143 ValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPhe 162
          |||:||                        ::|||||||||         :::||:|
Db    300 GTGATGGATGTCGTCGAATATTTCCGAACCGGTGGGAGTTTGAGGAGGAAGCTAGTGCTTTT 241

Qy    163 GlnGluGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThr 182
          |||||||                        |||||||||             ||||||
Db    240 CAGGAACACAGGAAAATGATGGAAAAATCCCTGCTATTGATGACAAGAAAATGATGGTTGACA 181

Qy    183 GlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleIleLysValLeu 202
          |||||||                        |||||||||||||||||
Db    180 GGACTTCAGTTAAAATTGGGGCGCCTCGTCTCTGAAAAATCTACGAATATCATGTAAAACCTCTG 121

Qy    203 GlnGlnGlyHisPheGluAspAsp 210
          |||                      :::::::::
Db    120 CAGACAAAGCATTTAAAGAACAAC 97
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:49:56 ; Search time 3295.9 seconds
(without alignments)
2853.675 Million cell updates/sec

Title: US-09-976-740-7
Perfect score: 1170
Sequence: 1 EERVLEKEEEEDDDEDDEDEE..........HIKVLQQGHFEDDPDGFLG 217

Scoring table: BLOSUM62

Xgapop	10.0 ,	Xgapext	0.5		
Ygapop	10.0 ,	Ygapext	0.5		
Fgapop	6.0 ,	Fgapext	7.0		
Delop	6.0 ,	Delext	7.0		

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xip
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -QFMT=fastap -SUFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1_9705 @runat_10032004_094548_19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pri:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: gb_fun:*
17: gb_hum:*
18: gb_in:*
19: gb_mu:*
20: gb_Om:*
21: gb_Or:*
22: gb_ov:*
23: gb_pat:*
24: gb_ph:*
25: gb_pl:*
26: gb_ro:*
27: gb_sts:*
28: gb_un:*

GenEmbl:*
29: em_vi:*
30: em_hum:*
31: em_inv:*
32: em_htg_inv:*
33: em_htg_other:*
34: em_htg_mus:*
35: em_htg_pln:*
36: em_htg_rod:*
37: em_htg_mam:*
38: em_htg_vrt:*
39: em_sy:*
40: em_htgo_hum:*
41: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1170	100.0	982	9	BC007384	BC007384 Homo sapi
2	1170	100.0	1208	6	AR199535	AR199535 Sequence
3	1170	100.0	1208	6	AR374687	AR374687 Sequence
4	1170	100.0	1208	6	AR409322	AR409322 Sequence
5	1170	100.0	1208	6	AX239573	AX239573 Sequence
6	1170	100.0	1208	6	BD056449	BD056449 Novel low
7	1170	100.0	1470	9	BC030129	BC030129 Homo sapi
8	1170	100.0	1614	9	AR409337	AR409337 Sequence
9	1170	100.0	1614	6	AX239602	AX239602 Sequence
10	1170	100.0	1617	6	AY453840	AY453840 Homo sapi
11	1047.5	89.5	1362	6	AR199531	AR199531 Sequence
11	1047.5	89.5	1362	6	AR374683	AR374683 Sequence
12	1047.5	89.5	1362	6	AR409318	AR409318 Sequence
13	1047.5	89.5	1362	6	AX239569	AX239569 Sequence
14	1047.5	89.5	1362	4	AY453841	AY453841 Oryctolag
15	1047.5	89.5	2561	6	AR409339	AR409339 Sequence
16	1047.5	89.5	1422	6	AR199532	AR199532 Sequence
17	1047.5	89.5	1422	6	AR374684	AR374684 Sequence
18	1047.5	89.5	1422	6	AR409319	AR409319 Sequence
19	1047.5	89.5	1422	6	AX239570	AX239570 Sequence
20	1047.5	89.5	1422	6	BD056446	BD056446 Novel low
21	1047.5	89.5	1617	6	AR199530	AR199530 Sequence
22	1047.5	89.5	1617	6	AR374682	AR374682 Sequence
23	1047.5	89.5	1617	6	AR409317	AR409317 Sequence
24	1047.5	89.5	1617	6	AX239568	AX239568 Sequence
25	1047.5	89.5	1617	2	BD056444	BD056444 Novel low
26	1047.5	89.5	2560	4	AC079562	AC079562 Mus muscu
27	1047.5	89.5	2561	6	AR409339	AR409339 Sequence
28	1047.5	89.5	2561	6	AX239605	AX239605 Sequence
29	1036.5	88.6	12425	6	AR409341	AR409341 Sequence
30	1036.5	88.6	12425	6	AX239607	AX239607 Sequence
31	1036.5	88.6	237931	2	AC022098	AC022098 Homo sapi
32	1036.5	88.6	215265	2	AC134005	AC134005 Rattus no
33	977.5	83.5	279020	2	AC133803	AC133803 Rattus no
34	930	79.5	140795	2	AC079562	AC079562 Mus muscu
35	930	79.5	218687	2	AC079501	AC079501 Mus muscu
36	882.5	75.4	263957	2	AC120697	AC120697 Rattus no
37	811	69.3	1134	6	BD275342	BD275342 49 Human
38	390	33.3	425	6	AR418294	AR418294 Sequence
39	390	33.3	425	6	BD113847	BD113847 EST and e
40	305.5	26.1	1566	9	AX714534	AX714534 Sequence
41	305.5	26.1	1566	9	AK056937	AK056937 Homo sapi
42	300	25.6	1957	6	AX322741	AX322741 Sequence
43	285	24.4	1066	9	AX274908	AX274908 Sequence
44	285	24.4	1510	9	BC037973	BC037973 Homo sapi
45	285	24.4	1601	6	AR339147	AR339147 Sequence

RESULT 1   ALIGNMENTS

```
LOCUS       BC007384                 982 bp    mRNA    linear   PRI 16-SEP-2003
DEFINITION  Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
            IMAGE:3677194), partial cds.
ACCESSION   BC007384
VERSION     BC007384.2  GI:33988219
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 982)
AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE       Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE     22388257
PUBMED      12477932
REFERENCE   2  (bases 1 to 982)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAY-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 20, 2003 this sequence version replaced gi:13938477.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 24 Row: g Column: 10.
FEATURES             Location/Qualifiers
     source          1..982
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677194"
                     /tissue_type="Lymph, Burkitt lymphoma"
                     /clone_lib="NIH_MGC_8"
                     /lab_host="DH10B-R"
                     /note="vector: pOTB7"
     gene            <1..982
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
     CDS             <1..711
                     /gene="LOC90378"
```

```
misc_feature                    /gene="LOC90378"
                                /codon_start=1
                                /product="LOC90378 protein"
                                /protein_id="AAH07384.2"
                                /db_xref="GI:33988220"
                                /db_xref="LocusID:90378"
                                /translation="PGRAPPAASARPSRSKRGGEERVLKEEEEDDDEDEEDDDVSE
                                GSEVPEEDRPAGAOHHQLNGERGDPQOSAKERVKEEWTPCGHGQGQDDGRGPAPGSGTPGV
                                FSMAAMNKEGGTASVAITGPDSPSPVPLPPGKPALPGADGTPPGCPPGRKEKPSDPVEW
                                TVMDVVEYFIEAGFPEQATVAFOBOEIDGKSLLLMQRTDVITGLSIRLGPALKIYEHHI
                                KVLQQGHFEDDDPDGFLG"
                                /note="SAM; Region: Sterile alpha motif. Widespread domain
                                in signaling and nuclear proteins. In EPH-related
                                tyrosine kinases, appears to mediate cell-cell initiated
                                signal transduction via the binding of SH2-containing
                                proteins to a conserved tyrosine that is phosphorylated.
                                In many cases mediates homodimerisation"
                                /db_xref="CDD:smart00454"
```

```
ORIGIN
```

```
US-09-976-740-7 (1-217) x BC007384 (1-982)

Alignment Scores:
Pred. No.:
Score:                      1170.00
Percent Similarity:         100.00%
Best Local Similarity:      100.00%
Query Match:                100.00%
DB:                         9
```

```
Qy    1 GluGluArgValLeuLysGluGluGluGluGluGluAspAspAspGluAspGluGlu 20
Db   58 GAAGAGCGAGTACTTGAAGAAGAAGAGGAAGAAGAGAGATGATGAAGATGAAGAGGAA 117

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
Db  118 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCTTCCTGCAGGTGCCCAGCAC 177

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluGluTrpThr 60
Db  178 CACCAGCTTAACGGCGAGCGGGGAGACCCTAGAAGTGCCAAGGAGAGGGTCAAGGAGGTGACC 237

Qy   61 ProCysGlyProHisGlnGlyGlnAspAspGlyArgGlyProAlaProGlySerGlyThr 80
Db  238 CCCTGCGGACCCGACCCAGGGCCAGGGCCAGGATGAAGGCCGGGGCCCAGGCAGCCGCACC 297

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
Db  298 CGGCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGGTTCGTTGCACC 357

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db  358 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC 417

Qy  121 AspGlyThrProProGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
Db  418 GACGGGACACCCCTTTGGCCGTGCTCCTCCCGGGCGCAAAGGAGAAGCCATCTGACCCGGTCGAG 477

Qy  141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
Db  478 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCCACA 537

Qy  161 AlaPheGlnGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db  538 GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTTCTCATGCAGCGCACAGATGTG 597

Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
Db  598 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAAATCTACGAGCACCACATCAAG 657

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db   658 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCTTCTTAGGC 708

RESULT 2
Db AR199535
LOCUS   AR199535   1208 bp   DNA   linear   PAT 20-APR-2002
DEFINITION   Sequence 16 from patent US 6355451.
ACCESSION   AR199535
VERSION   AR199535.1 GI:20249609
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 16 12-MAR-2002;
FEATURES   Location/Qualifiers
     source   1..1208
                     /organism="unknown"
                     /mol_type="unassigned DNA"

ORIGIN

US-09-976-740-7 (1-217) x AR199535 (1-1208)

Alignment Scores:
Pred. No.:
Score: 1.77e-54   Length: 1208
Percent Similarity: 1170.00   Matches: 217
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                        Gaps: 0

Qy   1 GluGluArgValLeuGluThrLysGluGluGluGluAspAlaAspGluAspGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGCGAGTACTTGAGAAAGAAGAAGAAGATGATGATGCAGATGAAGATGAAGAA 60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGGCTCGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120

Qy   41 HisGlnLeuAsnGlyValLysArgGlyTyrProGlnSerAlaLysValLysGluThrThr 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CACCAGCTTAACGGCGTGAAGCGGGGACCTCAGAGTGCCAAGGTCAAGGAGACTGGACC 180

Qy   61 ProCysGlyProHisGlnGlnAspGluGluGlyArgGlyTyrProAlaProGlySerGlyThr 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CCCTGCGGACCGCACCAGGGCGGCGGAGGAGGTCAAGGAGGACTGGACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGGACAGCTTCTGTTGCCACC 300

Qy 101 GlyProAspSerProSerProValProLeuProProGlyLysProGlyLysProGlyAla 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGGCAAACCTGGGGCC 360

Qy 121 AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACGGGACCCCCTTTGGCTGTCCTCCCGGCCGCGGCAAAGAGAAGCCATCTGATCCCGTCGAG 420

Qy 141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TGGACCGTGATGGATGTCGTGGAATATTTCACTGAGGCTGGATTCCCCGAGCAGGCGACA 480

Qy 161 AlaPheGlnGlyGluIleIleAspGlyLysSerLeuLeuMetGlnArgThrAspVal 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GCTTTCCAAGGAGAGATTATTGATGGGCAAAATCTTTGCTGTCATCGCAGCGACAGATGTG 540

Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CTCACCGGCCTGTCCATCCGGCTCCGGGCCCCAGCCCTGAAAAATCTACGAGCACCATCAAG 600

Qy 201 ValLeuGlnGlnGlyHisPheGluAspAspAspProMetGlyPheLeuGly 217
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCTTCTTAGGC 651

RESULT 3
Db AR374687
LOCUS   AR374687   1208 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION   Sequence 16 from patent US 6605588.
ACCESSION   AR374687
VERSION   AR374687.1 GI:40077502
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 16 12-AUG-2003;
FEATURES   Location/Qualifiers
     source   1..1208
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN

US-09-976-740-7 (1-217) x AR374687 (1-1208)

Alignment Scores:
Pred. No.:
Score: 1.77e-54   Length: 1208
Percent Similarity: 1170.00   Matches: 217
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                        Gaps: 0

Qy   1 GluGluArgValLeuGluThrLysGluGluGluGluAspAlaAspGluAspGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGCGAGTACTTGAGAAAGAAGAAGAAGATGATGATGCAGATGAAGATGAAGAA 60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGGCTCGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120

Qy   41 HisGlnLeuAsnGlyValLysArgGlyTyrProGlnSerAlaLysValLysGluThrThr 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CACCAGCTTAACGGCGTGAAGCGGGGACCTCAGAGTGCCAAGGTCAAGGAGACTGGACC 180

Qy   61 ProCysGlyProHisGlnGlnAspGluGluGlyArgGlyTyrProAlaProGlySerGlyThr 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CCCTGCGGACCGCACCAGGGCGGCGGAGGAGGTCAAGGAGGACTGGACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGGACAGCTTCTGTTGCCACC 300

Qy 101 GlyProAspSerProSerProValProLeuProProGlyLysProGlyLysProGlyAla 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGGCAAACCTGGGGCC 360

Qy 121 AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GACGGGACCCCCTTTGGCTGTCCTCCCGGCCGCGGCAAAGAGAAGCCATCTGATCCCGTCGAG 420

Qy 141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TGGACCGTGATGGATGTCGTGGAATATTTCACTGAGGCTGGATTCCCCGAGCAGGCGACA 480

Qy 161 AlaPheGlnGlyGluIleIleAspGlyLysSerLeuLeuMetGlnArgThrAspVal 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GCTTTCCAAGGAGAGATTATTGATGGGCAAAATCTTTGCTGTCATCGCAGCGACAGATGTG 540

Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CTCACCGGCCTGTCCATCCGGCTCCGGGCCCCAGCCCTGAAAAATCTACGAGCACCATCAAG 600

Qy 201 ValLeuGlnGlnGlyHisPheGluAspAspAspProMetGlyPheLeuGly 217
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCTTCTTAGGC 651

Left column

```
Db  541 CTCACCGGCGCCTGTCCATCCGCTCCGGGCCCAGCCCTGAAAATCTACGAGCACCACATCAAG 600

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db  601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

RESULT 4

```
AR409322
LOCUS       AR409322              1208 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6632923.
ACCESSION   AR409322
VERSION     AR409322.1  GI:40160110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 16 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

US-09-976-740-7 (1-217) x AR409322 (1-1208)

Alignment Scores:
```
Pred. No.:
Score:                 1.77e-54
Percent Similarity:    1170.00        Matches:       217
Best Local Similarity: 100.00%        Conservative:  0
Query Match:           100.00%        Mismatches:    0
                       6              Indels:        0
                                      Gaps:          0
```

```
Qy    1 GluGluArgValLeuGluHisLysGlyGluGlyGluAspAlaProGlyGluGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGCGAGTACTTGAGAAAGAAGAAGAATGATGAGTGAAGAGATGAAGAA 60

Qy   21 AspAspValSerGlyLySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCCGCACCAC 120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGlyProAlaGlyThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGCGAGCGCGGGACCTCAGAGTGCCAAGGAGGTCCAAGGATGGAC 180

Qy   61 ProCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGlySerGlyThr 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCGCACCAGGGGCCAGATGAAGGGCGGGGGCCAGCGCCCACGGGCGACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCAC 300

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GGGCCAGACTCCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGC 360

Qy  121 AspGlyThrProPheGlyCysProGlyValArgGlyLysGluProSerAspProValGlu 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACGGGACCCCCTTTGGCTGTCCTCCCGGCGCAAAGAACAGCCATTCTGATCCCGTCGAG 420

Qy  141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TGGACCGTGATGGATGTCGTGGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA 480

Qy  161 AlaPheGlnGlnGlyHisGluAspAspAspProAspGlyPheLeuGly 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCTTTCCAAGAGCAGGGAAAATTGATCGGCCAAATCTTTGCTGCTCATGCAGCCAGATGTG 540
```

Right column

```
Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTCACCGGCGCCTGTCCATCCGCTCCGGGCCCAGCCCTGAAAATCTACGAGCACCACATCAAG 600

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db  601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

RESULT 5

```
AX239573
LOCUS       AX239573              1208 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 16 from Patent WO0164874.
ACCESSION   AX239573
VERSION     AX239573.1  GI:15797257
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A1 16 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             <1..654
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC88296.1"
                     /db_xref="GI:15797258"
                     /db_xref="REMTREMBL:CAC88296"
                     /translation="EERVLEKEEEDDEDEDDEDEDDVSEGSEVPESDRPAGAQHQLN
                     GERGPQSAKERVKEWTPCGPHQGQDGGRGPAPGSGTRQVPRSMAAMNKEGGTASVATGP
                     DSPSPVPLPGKPALPGADGTPFGCPGVRGKEKPSDPVEWTVMDVVEYFTEAGFPEQAT
                     AFQEQEIDGKSLILMQRTDVLTGLSIRLGPALKIYEHHIKVLQQGHFEDDDPDGFLG"
ORIGIN
```

US-09-976-740-7 (1-217) x AX239573 (1-1208)

Alignment Scores:
```
Pred. No.:
Score:                 1.77e-54
Percent Similarity:    1170.00        Matches:       217
Best Local Similarity: 100.00%        Conservative:  0
Query Match:           100.00%        Mismatches:    0
DB:                    6              Indels:        0
                                      Gaps:          0
```

```
Qy    1 GluGluArgValLeuGluHisLysGlyGluGlyGluAspAlaProGlyGluGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGCGAGTACTTGAGAAAGAAGAAGAATGATGAGTGAAGAGATGAAGAA 60

Qy   21 AspAspValSerGlyLySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCCGCACCAC 120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGlyProAlaGlyThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGCGAGCGCGGGACCTCAGAGTGCCAAGGAGGTCCAAGGATGGAC 180

Qy   61 ProCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGlySerGlyThr 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCGCACCAGGGGCCAGATGAAGGGCGGGGGCCAGCGCCCACGGGCGACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCAC 300

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCAC 360
```

US-09-976-740-7 (1-217) x BD056449 (1-1208)

```
Qy          1 GluGluArgValLeuGlyLysGluGlyAspAlaAspAlaspGluAspGluGlu  20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAGAGAGGGAGGTACTTGAAAAGAAGAAGATGATGATGAAGATGAAGAA  60
```

ORIGIN

Alignment Scores:
Pred. No.:
Score: 1,776-54
Percent Similarity: 1170.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 1208
Matches: 217
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

FEATURES Location/Qualifiers
source 1..1208
  /organism="Aequorea victoria"
  /mol_type="genomic DNA"
  /db_xref="taxon:6100"

FH Key Location/Qualifiers
CC Topology: Linear;
CC Strandedness: Single;
PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC
PC A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC
PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
PF 26-NOV-1997 JP 199524870
PD 29-MAY-2001
PN JP 200506983-A/7

COMMENT BOSTON HEART FOUNDATION INC
Patent: JP 200506983-A 7 29-MAY-2001;
diagnosing and treating atherosclerosis
Novel low density lipoprotein binding proteins and their use in

JOURNAL

TITLE Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis.

AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.

REFERENCE 1 (bases 1 to 1208)

ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.

SOURCE Aequorea victoria

KEYWORDS JP 200506983-A/7.

VERSION BD056449.1 GI:22602055

ACCESSION BD056449

DEFINITION Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis..

LOCUS BD056449   1208 bp   DNA   linear   PAT 27-AUG-2002

RESULT 6

```
Db   601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGAACCCCGATGGCTTCTTAGGC 651

Qy   201 ValLeuGlnGlyHisPheGluAspAspAspGlyPheLeuGly 217
Db   541 CTCACCGGCCTGTTCCATCCGCCTGGGCCAGCCCTGAAAATCTACGACACCATCAAG 600

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyTyrProAlaLeuLysIleTyrGluHisHisIleLys 200
Db   481 GCTTTCCAAGCAGCAGGAAATTGATGGCAAATCTTTGCTCATGCCAGCGCGACAGATGTG 540

Qy   161 AlaPheGlnGluGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db   421 TGGACCGTGAGGATGGTCGTTGAATATTTTACTGAGGCTGGGATTCCCGGAGCAGTGGGACA 480

Qy   141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyIleProGluGlnAlaThr 160
Db   361 GACGGGACCCCCTTTGGCGTTCTCCCCGGGGCGAAAGAAGAGAAGCCATCTGATCCCGTCGAG 420

Qy   121 AspGlyThrProPheGlyCysProGlyAlaArgLysGluLysProSerAspProValGlu 140
Db   121 CACCAGCTTAACGGCGGGAGGAGGGGTCCTCGAGGTGCCAAGGAGTCAAGGAGTGGGAC 180

Qy    21 AspAspValSerGlyLysGluValProGluSerArgProAlaGlyAlaGlnHis 40
Db    61 GATGATGTGTCAGGAAGGGTTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120
```

```
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE     22388257
PUBMED      12477932
REFERENCE   2  (bases 1 to 1470)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (07-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:22535615.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC);
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 15 Row: m Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction.
FEATURES             Location/Qualifiers
     source          1..1470
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:39436 IMAGE:3943601"
                     /tissue_type="Lung, small cell carcinoma"
                     /clone_lib="NIH_MGC_7"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene            <1..1470
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
     CDS             <1..890
                     /gene="LOC90378"
                     /codon_start=3
                     /product="LOC90378 protein"
                     /protein_id="AAH30129.1"
                     /db_xref="GI:33871479"
                     /db_xref="LocusID:90378"
                     /translation="GAARPVSLREVVRYLGGSGSGGSGGAGGRLTRGRVQGLLEEAAAARGRL
                     ERTRLGALALPRGRPGRAPPAASARPSRSRKGGGEERVLEKEEEDEDDEDEEDVS
                     EGSSVPESDRPAGAQHQLNGERGPQSAKERVKEWTPCGPHGGDEDCERGRPAPGGSGTRQ
                     VFSMAAANKEGGTIASVATGPDSPSPVPLPPGKPALPGADGTPFGCPGPGRKEKPSDPVE
                     WTVMDVVFYFTEAGPPEQATAFQEEIDGKSLLLMQRDVIIGLSIRLGPALKIYEHH
                     IKVLQQGHFEDDPDGFLG"
     misc_feature    648..848
                     /gene="LOC90378"
                     /note="SAM; Region: Sterile alpha motif. Widespread domain
                     in signalling and nuclear proteins. In EPH-related
                     tyrosine kinases, appears to mediate cell-cell initiated
                     signal transduction via the binding of SH2-containing
                     proteins to a conserved tyrosine that is phosphorylated.
                     In many cases mediates homodimerisation"
                     /db_xref="CDD:smart00454"
ORIGIN
```

```
Alignment Scores:
Pred. No.:                            2.14e-54
Score:                                1170.00
Percent Similarity:                   100.00%     Matches:        217
Best Local Similarity:                100.00%     Conservative:     0
Query Match:                          9            Mismatches:       0
DB:                                                Indels:           0
                                                   Gaps:             0
                                                                  Length:  1470
                                                                  Matches:  217

Qy       1 GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluGlu  20
Db     237 GAAGAGCGAGTACTTGAGGAAAGAGAAGGAAGAAGATGAAGATGAAGAGATGAAGAA 296

Qy      21 AspAspValSerGlyLysGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
Db     297 GATGATGTGTCAGGAGGCCTCTGAAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 356

Qy      41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
Db     357 CACCAGCTTAACGGCGAACGCGGGCCACCCCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 416

Qy      61 ProCysGlyProHisGlnGlyGlnAspGluGlyAlaGlyProAlaProGlySerGlyThr 80
Db     417 CCCTGCGGACCCCACCAGGGGCCAGGATGAAGACGGGCGGGGGGCCAGCGCCACC 476

Qy      81 ArgGlnValPheSerMetAlaAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
Db     477 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTTGCCACC 536

Qy     101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db     537 GGGCCAGACTCCCCGTCCCCGGGTGCCTTTGCCCCAGGCAAACCAGCCCTACCTGGGGCC 596

Qy     121 AspGlyThrProPheGlyCysProGlyProGlyArgLysGluLysProSerAspProValGlu 140
Db     597 GACGGGACCCCCTTTGGCGTGTCCTCCCGGCGCCAAAGAGAAGCCATCTGATCCCGTGGAG 656

Qy     141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyProProGluGlnAlaThr 160
Db     657 TGGACCGTGATGGATGTGGTCGAATATTTTACTGAGGCTGGACCCCCGGAGCAGGCCACA 716

Qy     161 AlaPheGlnGluGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db     717 GCTTTCCAAGAGGCAGGAGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG 776

Qy     181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
Db     777 CTCACCGGCCTGTCCATCCGCCTCGGGCCCAGCCCCCTGAAAAATCTACGAGCACCATCAAG 836

Qy     201 ValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly 217
Db     837 GTGCTTCAGCAAGGGCACTTTGAGGATGATCCACCCCGATGGCTTCTTAGGC 887
```

```
LOCUS       AR409337                  45 bp    DNA        linear   PAT 18-DEC-2003
DEFINITION  Sequence 45 from patent US 6632923.
ACCESSION   AR409337
VERSION     AR409337.1  GI:40160125
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown
            Unclassified.
REFERENCE   1  (bases 1 to 1614)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 45 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..1614
                     /organism="unknown"
```

Left column

```
JOURNAL    Patent: WO 0164874-A 45 07-SEP-2001;
           and treating atherosclerosis
TITLE      Low density lipoprotein binding proteins and their use in diagnosing
AUTHORS    Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
REFERENCE  1
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Homo sapiens
SOURCE     Homo sapiens (human)
KEYWORDS   .
VERSION    AX239602.1  GI:15797275
ACCESSION  AX239602
DEFINITION Sequence 45 from Patent WO0164874.
LOCUS      AX239602      1614 bp    DNA    linear   PAT 26-SEP-2001
AX239602
RESULT 9
```

```
ORIGIN                            /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:
Score:                    2.34e-54
                                    Length:         1614
                                    Matches:        217
Percent Similarity:       100.00%   Conservative:   0
Best Local Similarity:    100.00%   Mismatches:     0
Query Match:              100.00%   Indels:         0
DB:                       6         Gaps:           0

US-09-976-740-7 (1-217) x AR409337 (1-1614)

Qy    1   GluGluArgValLeuGlyLeuGlyLeuGlyLeuGluAspAlaSerProGluAspGluGlu  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  964   GAAGAGCGAGTACTTGGAAGAAGAGGAAGAAGATGATGAAGACATGAAGAGATGAAGAA  1023

Qy   21   AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis  40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024   GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCAGGTGCCCAGCAC   1083

Qy   41   HisGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLeuAlaLysGluArgValLysGlyTrpThr  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084   CACCAGCTTAACGGCCGAGCGGGGGGACCTCAGAGTGCCAAGGAGGGTCAAGGAGGGTGACC  1143

Qy   61   ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1144   CCCTGCGGACCCCACCAGGGCCAGGACGATGAAGGGCGGGGGCCAGGGCCGGGCGGCACC  1203

Qy   81   ArgGlnValPheSerMetAlaAlaAsnLysGluGlyGlyThrAlaSerValAlaThr  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1204   CGCCAGGTGTTCTCAATGGCAGCCAATAAGGAAGGGGGAACAGCTTCTGTTGCCACC  1263

Qy  101   GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1264   GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC  1323

Qy  121   AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1324   GACGGGACACCCCTTTGGCGTGTCCCCCGGGCGTGGTAAGCCATCTGATCCCGTCGAG  1383

Qy  141   TrpThrValMetAspValAlaGluTyrPheThrGluAlaGlyPheProGlyAlaIleThr  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1384   TGGACCGTGATGGATGTCGCTGAATATTTTACTGAGGCTGGATTCCCGGGAGCAATTACT  1443

Qy  161   AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1444   GCTTTCCAAGAGCAGGAAATTGATGGCAAAATCTTTACTCATGCGCCGACGATGTG  1503

Qy  181   LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1504   CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCAGCCCTGAAAATCTACGAGCACCAC  1563

Qy  201   ValLeuGlnGlnHisPheGluAspAspProAspGlyPheLeuGly  217
          ||||||||||||||||||||||||||||||||||
Db 1564   GTGCTTCAGCAAGGCCACTTTGAGGATGATCCCGATGGCTTCTTAGGC  1614
```

Right column

```
                    Boston Heart Foundation, Inc. (US)

FEATURES          Location/Qualifiers
     source       1..1614
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
     CDS          1..>1614
                  /note="unnamed protein product"
                  /codon_start=1
                  /protein_id="CAC88299.1"
                  /db_xref="GI:15792276"
                  /db_xref="REMTREMBL:CAC88299"
                  /translation="MAGPPALPPETAAAATTNAAAASSSAASPHYQEWYLLDTIDSLRS
                  RKARPDLRRICRMVRRHGCPEPERTRAELEKLIQQRAVLRVSYKGSISYRNAARVQPP
                  RRGATPPAPPRRAPRGAPAPAAAAAAPPTPFAPPPRAPPPPPAVVAAAAPARARAAATAPP
                  SPGPAQPGPRAQRAAPLAAPPRAAPPAVVAPPAGPPRRAPPPAVVAAREPPLPPPPQPP
                  APPQQQOPPPPGQOPPPEGGAVRAGGAARPVSLREVVRYLGSSGGAGGRLTRGRVGGL
                  LEEBAAARGRLERTRLGALALPRGDRGRAPPAASARSRSRKGGEERVLEKEEEBDD
                  DEDEDEEDDVSESEVPESDRPAGAQHHQLNGERGPQSAKERVKEWTPCGPHQGQDEG
                  RGPAPGSGTRQVFSMAANKEGGTASVATGPDSPSPVPLPPGKPALPGADGTPFGCPP
                  GRKEKPSDPVEWTVMDVVEYFTEAGFPGAIQEQEIDGKSLLLMQRTDVLITGLSIR
                  LGPALKIYEHHIKVLQQHFEDDPDGFLG"

US-09-976-740-7 (1-217) x AX239602 (1-1614)

Alignment Scores:
Pred. No.:
Score:                    2.34e-54
                                    Length:         1614
                                    Matches:        217
Percent Similarity:       100.00%   Conservative:   0
Best Local Similarity:    100.00%   Mismatches:     0
Query Match:              100.00%   Indels:         0
DB:                       6         Gaps:           0

Qy    1   GluGluArgValLeuGlyLeuGlyLeuGlyLeuGluAspAlaSerProGluAspGluGlu  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  964   GAAGAGCGAGTACTTGGAAGAAGAGGAAGAAGATGATGAAGACATGAAGAGATGAAGAA  1023

Qy   21   AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis  40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024   GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCAGGTGCCCAGCAC   1083

Qy   41   HisGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLeuAlaLysGluArgValLysGlyTrpThr  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084   CACCAGCTTAACGGCCGAGCGGGGGGACCTCAGAGTGCCAAGGAGGGTCAAGGAGGGTGACC  1143

Qy   61   ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1144   CCCTGCGGACCCCACCAGGGCCAGGACGATGAAGGGCGGGGGCCAGGGCCGGGCGGCACC  1203

Qy   81   ArgGlnValPheSerMetAlaAlaAsnLysGluGlyGlyThrAlaSerValAlaThr  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1204   CGCCAGGTGTTCTCAATGGCAGCCAATAAGGAAGGGGGAACAGCTTCTGTTGCCACC  1263

Qy  101   GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1264   GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC  1323

Qy  121   AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1324   GACGGGACACCCCTTTGGCGTGTCCCCCGGGCGTGGTAAGCCATCTGATCCCGTCGAG  1383

Qy  141   TrpThrValMetAspValAlaGluTyrPheThrGluAlaGlyPheProGlyAlaIleThr  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1384   TGGACCGTGATGGATGTCGCTGAATATTTTACTGAGGCTGGATTCCCGGGAGCAATTACT  1443

Qy  161   AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1444   GCTTTCCAAGAGCAGGAAATTGATGGCAAAATCTTTACTCATGCGCCGACGATGTG  1503

Qy  181   LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1504   CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCAGCCCTGAAAATCTACGAGCACCACATCAAG  1563
```

```
RESULT 10
AY453840

Db      AY453840

LOCUS           AY453840                1617 bp    mRNA    linear   PRI 03-DEC-2003
DEFINITION      Homo sapiens atherin mRNA, complete cds.
ACCESSION       AY453840
VERSION         AY453840.1  GI:38565528
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 1617)
  AUTHORS       Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
  TITLE         Atherin, a newly identified LDL-binding protein in human
                atherosclerotic lesions
  JOURNAL       Unpublished
REFERENCE       2  (bases 1 to 1617)
  AUTHORS       Deconinck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
  TITLE         Direct Submission
  JOURNAL       Submitted (30-Oct-2003) Harvard-MIT Division of Health Sciences and
                Technology, Boston Heart Foundation, 139 Main Street, Cambridge, MA
                02142, USA
FEATURES             Location/Qualifiers
     source          1..1617
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.12"
     CDS             1..1617
                     /note="LDL-binding protein; co-localizes with LDL in very
                     early human atherosclerotic lesions"
                     /codon_start=1
                     /product="atherin"
                     /protein_id="AAR24087.1"
                     /db_xref="GI:38565529"
                     /translation="MAGPPALPPETAAAATTAAAASSAASAPHYQEWILDTIDSLRS
                     RXAPDLERICRMVRRHGPEPERTRAELEKLIQQRAVLRVSYKGISYRNAARVQPP
                     RGATPPPRPPAAPLAAPPPAPAAPPAVAPPDGRAPAAPVSLREVRRYLGGSGGGGRLRPGRGVGL
                     SPGPAQPGPRAQRAAPLAAPPAAPPAPAVAAREPPLPPPQP
                     APPQQOPPPQPPQPPQPPEGGAVRAGGAARPVSLREVRRYLGGSGGGGRLRPGRVGL
                     LEEEAAARGRLERTRLGALALTPRGDRFGRAPPAASARPSRKRGGEERVLKEEEEDD
                     DEDEDEDVSEGSEVPESDRPAGAOHIQLNGRGPQSAKERVKEWTPCGPHGQGDEG
                     RGPAPGGSTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPGKPALPGADGTPFGCPP
                     GRXEXPSDPVEWTVMDVVEYFTEAGFPPQOAIAPQEQEIDGKSLLLMQRITDVLTGLSTR
                     LGPALKIYEHHIKVLQQGHFEDDPDGFLG"
ORIGIN
```

```
RESULT 11
AR199531

Db      AR199531

LOCUS           AR199531                1362 bp    DNA     linear   PAT 20-APR-2002
DEFINITION      Sequence 12 from patent US 6355451.
ACCESSION       AR199531
VERSION         AR199531.1  GI:20249605
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1362)
  AUTHORS       Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE         Low density lipoprotein binding proteins and their use in
                diagnosing and treating atherosclerosis
  JOURNAL       Patent: US 6355451-A 12 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..1362
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
```

Left column alignments (US-09-976-740-7 vs AY453840):

```
Qy   201 ValLeuGlnGlnGlyHisPheGluAspProAspGlyPheLeuGly 217
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 1614

US-09-976-740-7 (1-217) x AY453840 (1-1617)

Alignment Scores:
  Pred. No.:                               10
  Score:                             1170.00
  Percent Similarity:                100.00%        Percent Identity:        100.00%
  Best Local Similarity:             100.00%
  Query Match:                             9

Qy     1 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluAspGluGlu 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 GAAGAGCGAGTTACTTGAGAAAAGAAGAAGAAGAGATGAATGATGAAGATGAAGATGAAGAA 1023

Qy    21 AspAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCAGCTGCCCAGCAC 1083

Qy    41 HisGlnLeuAsnGlyArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1084 CACCAGCTTAACGGCGAGGCGGGGGGGGGGGACTTCAGAGTGCCAAGGAGAGGGG... 1143
```

Right column alignments (US-09-976-740-7 vs AR199531):

```
Qy    61 ProCysGlyProHisGlnGlyTyrGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1144 CCCTGCGGGACCCGGCACCAGGGGTACCAGGATGAAGGGCGGGGGCGGGCGGTCGGGTCACC 1203

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1204 CGGCAGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGAGGCACAGCTTCGGTTGCCACC 1263

Qy   101 GlyProAspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAla 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1264 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCAGCCAAACCAGCCCTACCTGGGGCC 1323

Qy   121 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1324 GACGGGACCCCCTTTGGCTGTCCGCCCGGGCGCAAAGAGAAGCCATCTGATCCCGTCGAG 1383

Qy   141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProProGlnAlaThr 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1384 TGGACCGTGATGGATGTGGTCGAATATTTCACTGAGGCTGGATTCCCGCCGCAGGCCACA 1443

Qy   161 AlaPheGlnGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1444 GCTTTCCAAGAGCAGGAAATTGATGGCAAAAGTCTTTGCTCATGCAGCGCACAGAGATGTG 1503

Qy   181 LeuThrGlyLeuSerThrArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1504 CTCACCGGCCTGTCCACCCGCCTCGGGCCCGCAGCCCTGAAAAATCTTACGAGCACCATCAAG 1563

Qy   201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 1614

US-09-976-740-7 (1-217) x AR199531 (1-1362)

Alignment Scores:
  Pred. No.:                         7.08e-48
  Score:                             1047.50
  Percent Similarity:                  95.45%        Percent Identity:        89.53%
  Best Local Similarity:               88.64%
  Query Match:                             6

Qy     1 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluAspGluGlu 20
         ||||||||||||||||||| ||||||||||||::::|||||||||||||||||:::::
Db   964 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluAspGluGlu... 20

Qy    21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlyAla 38
         ||||      ::::::::::::||||||||||||:::::|||||||||||||||||||
Db    37 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAAGAGGACGAGGACGAC 96

Qy    21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
         ||||       ::::::::::::||||||||||:::::|||||||||||||||||
Db    97 GACGACGAGCGTCGTGTTCCGAGGGGTGCCCGAGAGCGGCAATCGTCCCGAGGGCG 156
```

RESULT 12

```
LOCUS           AR374683                1362 bp    DNA       linear   PAT 18-DEC-2003
DEFINITION      Sequence 12 from patent US 6605588.
ACCESSION       AR374683
VERSION         AR374683.1  GI:40077498
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1362)
  AUTHORS       Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE         Low density lipoprotein binding proteins and their use in
                diagnosing and treating atherosclerosis
  JOURNAL       Patent: US 6605588-A 12 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1..1362
                     /organism="unknown"
                     /mol_type="genomic DNA"
```

ORIGIN

Alignment Scores:
```
Pred. No.:
Score:                   7.08e-48
Score:                   1047.50
Percent Similarity:      95.45%          Length:          1362
Best Local Similarity:   88.64%          Matches:         195
Query Match:             89.53%          Conservative:    15
DB:                                      Mismatches:      7
                                         Indels:          3
                                         Gaps:            2
```

US-09-976-740-7 (1-217) x AR374683 (1-1362)

```
Qy   39  GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys  57
         |||||||||||||||       |||||||||||||||||||||::|||||||||||||||
Db  157  CAGCATCACCAGCTGAAATGGGGGGCGGAGCGCGGCCCCCAGAGCGCCAAGGAGCGGGTGCG  216

Qy   58  GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyLeuGlyGlyGlyProAlaProGly  77
         |:::|||
Db  217  GAGTGGTGTCGTGTGTGGCCCCCACCCTGGCCCCCAGGACGAAGGGGGGGGCCCCGGGGC  276

Qy   78  SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer  97
         |||
Db  277  AGTGGCACCCGCCCAGGTGTTCTCAATGGCGGCCCTTGAGTAAGGAGGGGATCAGCCTCT  336

Qy   98  ValAlaThrGlyHisProAspSerProSerProValProLeuProProGlyLysProAlaLeu  117
         ||||
Db  337  TCGACACCAGCGGGCGTTGACTCCCGCGTCCCCGTCCCCCGGGGGAGCCAGCCCTC  396

Qy  118  ProGlyAlaAspGlyThrProPheGlyTyrCysProProGlyArgLysGluLysProSerAsp  137
         |||
Db  397  CCAGGAGCCGGATGGGACCCCCTTTGGGCTGCCCGGGGGCAAAGAGAAGCCGGACAGAC  456

Qy  138  ProValGluTrpThrProValMetAspValAlaValGlyTyrPheThrGluAlaGlyProGlu  157
         |||
Db  457  CCCGGTGGAGTGGACAGTCATGGACGTGGCGGTGGGGGCTGACTTTACCGAGGCGGGTCCGGAG  516

Qy  158  GlnAlaThrAlaPheGlnGlyLeuSerIleArgLeuGlyProAlaLeuLeuLeuMetGlnArg  177
         |||
Db  517  CAAGCCACGGCCTTTCCAGGAGCACAGTCAGGAGGTCGTGGAGTACTTCACCCAGGCGGCTTCCCTGAG  576

Qy  178  ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLeuLysSerIleTyrGluHis  197
         |||
Db  577  ACCGGATGTCCTCACCGGCCTGTCCCATCCGCCTGGGGCCCAGCCGTTGAAAAATCTATGAGCAC  636

Qy  198  HisIleLysValLeuGlnGlnGlnHisPheGluAspAspAspProGlyPheLeuGly  217
         |||
Db  637  CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA  696
```

RESULT 13

```
LOCUS           AR409318                1362 bp    DNA       linear   PAT 18-DEC-2003
DEFINITION      Sequence 12 from patent US 6632923.
ACCESSION       AR409318
VERSION         AR409318.1  GI:40160106
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1362)
  AUTHORS       Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE         Low density lipoprotein binding proteins and their use in
                diagnosing and treating atherosclerosis
  JOURNAL       Patent: US 6632923-A 12 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..1362
                     /organism="unknown"
                     /mol_type="genomic DNA"
```

ORIGIN

Alignment Scores:
```
Pred. No.:
Score:                   7.08e-48
Score:                   1047.50
Percent Similarity:      95.45%          Length:          1362
Best Local Similarity:   88.64%          Matches:         195
Query Match:             89.53%          Conservative:    15
DB:                                      Mismatches:      7
                                         Indels:          3
                                         Gaps:            2
```

US-09-976-740-7 (1-217) x AR409318 (1-1362)

```
Qy    1  GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluGlu  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37  GAGGAGCGGGAGTGCTTGAAAAGGAGGAGGAGGAGGACGAGGAGGACGAC  96

Qy   21  AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla  38
Db   37  GAGGAGCGGGAGTGCTTGAAAAGGAGGAGGAGGAGGACGAGGAGGACGAC  96
```

RESULT 14

LOCUS   AX239569   1362 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION Sequence 12 from Patent WO0164874.
ACCESSION   AX239569
VERSION   AX239569.1 GI:15797249
KEYWORDS   .
SOURCE   Oryctolagus cuniculus (rabbit)
  ORGANISM Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density liprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 12 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1362
                     /organism="Oryctolagus cuniculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9986"
     CDS   <1..699
                     /codon_start=1
                     /note="unnamed protein product"
                     /protein_id="CAC88292.1"
                     /db_xref="GI:15797250"
                     /db_xref="REMTREMBL:CAC88292"
                     /translation="ASARAARNKRAGERVLEKEEEEEEEEDEDDDDDVVSEGGSEVP
                     ESDRPAGAQHHQLNGGERGPQTAKERAKEWSLCCGPHPGQEGCRGRGPAAGSGTRQVFSMA
                     ALSKEGGASSTTGPDSPSPVFLPFPGKPALPGADGTPFGPCPAGRKERPADPVEWTVMD
                     VVEYFTEAGFPEQATAFQEEIDGKSLLLMQRDTVLTGLSIRLGPALKIYEHHIKVLQ"

ORIGIN
Alignment Scores:
Pred. No.:
Score: 1047.50
Percent Similarity: 95.45%
Best Local Similarity: 88.64%
Query Match: 89.53%
DB:

Length: 1362
Matches: 195
Conservative: 15
Mismatches: 7
Indels: 3
Gaps: 2

Qy   21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
Db   97 GACGACGACGTCGTGTCTGTTCCGAGGGCTTCGGAGAGGTGCCCGAGAGCGATCGTCCGGCGGGTGCG 156

Qy   39 GlnHisHisGlnleuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
Db 157 CAGCATCACCAGCTGAATGGCGCGAGGCGGGGCCCCAGAACCCCAAGGAGCGGGCGAAG 216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyLysAlaspGluGlyArgGlyProAlaProGly 77
Db 217 GAGTGGTCGCGTGTCGCCCACCCTGGCAGAAGGGGGGGCCGCGCGGGC 276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
Db 277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGGAGGGGGGGGATCAGCCTCT 336

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProPheProGlyLysProAlaLeu 117
Db 337 TCGACCACCGGGGCCTGACTCCCCGGTCCCCGGGGAAGCCAGCCCTC 396

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProAlaGlyArgLysGluLysProSerAsp 137
Db 397 CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCAGCGGTTGAAAATCTATGAGCAC 456

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPhePheProGlu 157
Db 457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGGGC 516

Qy 158 GlnAlaThrAlaPheGlnGluGluIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 517 CAAGCCACGGCTTTCCAGGAGGAGATCGACGGGAAGTCCCTGCTCATGCAGCGC 576

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 577 ACCGATGTCCTCACCGGCCTGTCCATCCGGCTGGGGCCAGCGCTC 636

Qy 198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly 217
Db 637 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGACGGCTTCCTGGGA 696

RESULT 15

LOCUS   BD056445   1362 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis.
ACCESSION   BD056445
VERSION   BD056445.1 GI:22602051
KEYWORDS   JP 2001506983-A/3.
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 1362)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis

US-09-976-740-7 (1-217) x AX239569 (1-1362)

QGHFEDDPEGFLG"

Qy   1 GluGluArgValLeuGluLysGluGluGluGluGluAspAspAspAspGluAspGlu 20
Db   37 GAGGAGAGGGTGCTTGAAAAGGAGGAGGAGGAGGAGGAAGACGAC 96

Qy   21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
Db   97 GACGACGACGTCGTGTCTGTTCCGAGGGCTTCGGAGAGGTGCCCGAGAGCGATCGTCCGGCGGGTGCG 156

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
Db 157 CAGCATCACCAGCTGAATGGCGCGAGGCGGGGCCCCAGAACCCCAAGGAGCGGGCGAAG 216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyLysAlaspGluGlyArgGlyProAlaProGly 77
Db 217 GAGTGGTCGCGTGTCGCCCACCCTGGCAGAAGGGGGGGCCGCGCGGGC 276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
Db 277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGGAGGGGGGGGATCAGCCTCT 336

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProPheProGlyLysProAlaLeu 117
Db 337 TCGACCACCGGGGCCTGACTCCCCGGTCCCCGGGGAAGCCAGCCCTC 396

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProAlaGlyArgLysGluLysProSerAsp 137
Db 397 CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCAGCGGTTGAAAATCTATGAGCAC 456

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPhePheProGlu 157
Db 457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGGGC 516

Qy 158 GlnAlaThrAlaPheGlnGluGluIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 517 CAAGCCACGGCTTTCCAGGAGGAGATCGACGGGAAGTCCCTGCTCATGCAGCGC 576

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 577 ACCGATGTCCTCACCGGCCTGTCCATCCGGCTGGGGCCAGCGCTC 636

Qy 198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly 217
Db 637 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGACGGCTTCCTGGGA 696

```
JOURNAL      Patent: JP 2001506983-A 3 29-MAY-2001;
             BOSTON HEART FOUNDATION INC
COMMENT      PN   JP 2001506983-A/3
             PD   29-MAY-2001
             PF   26-NOV-1997 JP 199852487O
             PR   27-NOV-1996 US        60/031930, 03-JUN-1997 US        60/048547 PI
             ANN  M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
             A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08,   PC
             C07H21/00,
             PC   C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
FEATURES     Strandedness: Single;
             CC   Topology: Linear;
             FH   Key              Location/Qualifiers
source                  Location/Qualifiers
                        1. .1362
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

Alignment Scores:
Pred. No.:           7.08e-48
Score:               1047.50          Length:         1362
Percent Similarity:  95.45%           Matches:        195
Best Local Similarity: 88.64%         Conservative:   15
Query Match:         89.53%           Mismatches:     7
DB:                                   Indels:         3
                                      Gaps:           2

US-09-976-740-7 (1-217) x BD056445 (1-1362)

Qy    1 GluGluArgValLeuGlyLeuGluLysGluLeuGluAspAspAlaAspGluAspGluGlu 20
        ||||||||||||||||||||||||||||||||||||||||||||::::::::::::::::
Db   37 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGACACGAGGACGAGGACGAC 96

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspAArgProAlaGlyAla 38
        |||||       ||||||||||||||||||||||||||||||||||||||||||||::::
Db   97 GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGGGGTGCG 156

Qy   39 GlnHisHisGlnLeuAsn------GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
        |||||||||||||||        ||||||||||||||||||||:::||||||||||||||
Db  157 CAGCACCACCAGCTGAATGGGGGCGAGCGCGGCCCCAGAGCACGGCCAAGGAGCGGGCCAAG 216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly 77
        |||||||||||::::||||||||||||||||||||||||||||||||||||:::||
Db  217 GAGTGGACGCCGTGTGGGCCCCACCCTGGCCAGGAGGAAGGGCGGGGGCCCCGGGGGC 276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyValGlyThrLeuSer 97
        ||||||||||||||||||||||||||||||||||:::::|||||||||||||||||
Db  277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCCCAGGGGATCAGCCCTCT 336

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 TCGACCACCGGCGCCTGACTCCCCGTCCCCCGTGCCTTTGCCCCCGGGAGCCAGCCCTC 396

Qy  118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAsp 137
        |||||||||||||||||||||||||||||||:::::|||||||||::::||
Db  397 CCAGGAGCCGGATGGGAGCCCCTTTGGCTGCCCTCCCGGGGCGCAAAGAGAAGCCGGCGAC 456

Qy  138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyProGlu 157
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACGGAGGCGGGCTTCCCTGAG 516

Qy  158 GlnAlaThrAlaPheGlnGluGlnIleAspGlyLysSerLeuLeuMetGlnArg 177
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  517 CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGGAAGTCCCTGCTGCTCATGCAGCGC 576

Qy  178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  577 ACCGATGTCTCACCGGCCCTGTCCATCCGCCTGGGCCCAGCGTTGAAAAATCTATGAGCAC 636

Qy  198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProGlyPheLeuGly 217
        ||||||||||||||||||||||||||||:::::||||||||::::||||||
Db  637 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGACGATGACCCGGGAAAGCTTCCTGGGA 696
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 20:05:17 ; Search time 73.5728 Seconds
(without alignments)
1636.805 Million cell updates/sec

Title:
Perfect score: 1170
Sequence: 1 EERVLEKEEEDDDEDDEE..........HIKVLQQGHFEDDDPDGFLG 217

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: US-09-976-740-7

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Searched: 682709 seqs, 277475446 residues

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19564/app_query.fasta_1.1898
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1_235 @runat_10032004_094549_19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1170	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appl
2	1170	100.0	1208	4	US-09-517-849-16	Sequence 16, Appl
3	1170	100.0	1208	4	US-09-616-289-16	Sequence 16, Appl
4	1170	100.0	1614	4	US-09-616-289-45	Sequence 45, Appl
5	1047.5	89.5	1362	4	US-08-979-608A-12	Sequence 12, Appl
6	1047.5	89.5	1362	4	US-09-517-849-12	Sequence 12, Appl
7	1047.5	89.5	1362	4	US-09-616-289-12	Sequence 12, Appl
8	1047.5	89.5	1422	4	US-08-979-608A-13	Sequence 13, Appl
9	1047.5	89.5	1422	4	US-09-517-849-13	Sequence 13, Appl
10	1047.5	89.5	1422	4	US-09-616-289-13	Sequence 13, Appl
11	1047.5	89.5	1617	4	US-08-979-608A-11	Sequence 11, Appl
12	1047.5	89.5	1617	4	US-09-517-849-11	Sequence 11, Appl
13	1047.5	89.5	1617	4	US-09-616-289-11	Sequence 11, Appl
14	1047.5	89.5	2561	4	US-09-616-289-48	Sequence 48, Appl
15	1036.5	88.6	12425	4	US-09-616-289-50	Sequence 50, Appl
16	390	33.3	425	4	US-09-621-976-9791	Sequence 9791, Ap
17	285	24.4	1453	4	US-09-976-594-760	Sequence 760, App
18	285	24.4	1601	4	US-09-620-312D-638	Sequence 638, App
19	168.5	14.4	1933	4	US-08-974-380-1	Sequence 1, Appl
20	168.5	14.4	1933	4	US-09-546-977A-1	Sequence 1, Appl
21	168.5	14.4	1933	4	US-09-654-466-1	Sequence 1, Appl
22	154.5	13.2	3065	4	US-08-852-153-7	Sequence 7, Appl
23	153	13.1	3879	2	US-08-979-608A-31	Sequence 31, Appl
24	144	12.3	3327	2	US-09-517-849-31	Sequence 31, Appl
25	144	12.3	3255	2	US-08-852-153-5	Sequence 5, Appl
26	144	12.3	3255	2	US-08-852-153-1	Sequence 1, Appl
27	136	11.6	78	4	US-09-574-959A-6	Sequence 6, Appli
28	136	11.6	78	4	US-09-357-014-6	Sequence 6, Appli
29	136	11.6	78	2	US-09-188-930-30	Sequence 30, Appl
30	130.5	11.2	2481	2	US-08-894-998A-35	Sequence 35, Appl
31	123	10.5	3211	2	US-08-574-959A-8	Sequence 8, Appli
32	123	10.5	3211	2	US-09-357-014-8	Sequence 8, Appli
33	123	10.5	3901	2	US-09-574-959A-6	Sequence 6, Appli
34	123	10.5	3901	2	US-09-357-014-6	Sequence 6, Appli
35	122.5	10.5	1015	3	US-09-188-930-30	Sequence 30, Appl
36	122.5	10.5	1015	4	US-09-188-930-218	Sequence 218, App
37	121.5	10.4	1001	4	US-09-312-283C-218	Sequence 218, App
38	121.5	10.4	1015	3	US-09-312-283C-30	Sequence 30, Appl
39	121	10.3	13842	4	US-09-105-537-30	Sequence 30, Appl
40	121	10.3	36778	4	US-09-105-537-5	Sequence 5, Appli
41	121	10.3	38506	3	US-09-320-878-19	Sequence 19, Appl
42	121	10.3	38506	3	US-09-141-908-19	Sequence 19, Appl
43	121	10.3	38506	4	US-09-657-440-19	Sequence 19, Appl
44	120.5	10.3	2721	6	US-5215881-2	Patent No. 5215881
45	120.5	10.3	8438	1	US-07-945-283-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-979-608A-16
Sequence 16, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;
INFORMATION FOR SEQ ID NO: 16:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1208 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    FEATURE:
        NAME/KEY: Coding Sequence
        LOCATION: 1..651
;
US-08-979-608A-16
        SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Alignment Scores:
Pred. No.:
Score: 1.34e-86
Percent Similarity: 1170.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-08-979-608A-16

US-09-976-740-7 (1-217) x US-08-979-608A-16 (1-1208)

Qy   1 GluGluArgValLeuGluLysGlyGluGluGluGluAspAspAspAspGluGluAspGluGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAA 60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACCAGCTTAACGGCGGAGCGCGGGACCTCAGAGTCGCCAAGGAGAGGGTCAAGGAGTGGACC 180

Qy   61 ProCysGlyProHisGlnHisGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCGGCCCCGGGCAGCGGCCACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGluGlyThrAlaSerValAlaThr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCGTTGCCACC 300

Qy   101 GlyProAspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAla 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCCAGACTCCCCGTCCCCCGTGCCTTTCCCCCCAGGAAACCCAGCCCTACCTGGGGCC 360

Qy   121 AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGGGACCCCCTTTGGCTGTCCCCCGGGGCGCAAAGAAGGAAGCCATCTGAATCCCGTGGAG 420

Qy   141 TrpThrValMetAspValValGlnTyrPheThrGluIleAspAsnProGluGlnAlaThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGACCGTGATGGAGGTGGTGCAATATTTTACTGAGGCTTGGAATCCCGGAGCCAGGCAGCA 480

Qy   161 AlaPheGlnGluGlnLysGluAspGlyLysSerLeuLeuMetGlnArgThrAspVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTTTCCAAGAGCAGAAATTGATGGCAAAATCTTTGCTGCTCATCGAGCCACAGATGTG 540

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTCACCGGGCTCTGTCCATCCGCCTCGGGCCTGAAAATCTACGAGCACCACATCAAG 600

Qy   201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyTyrPheLeuGly 217
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGCTTCAGCAAGGCCACTTTGAGGAGGATGATGACCCGGATGGCTTCTTAGGC 651

; Patent No. 6605588
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2004
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/517,849
;   FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/979,608
;   FILING DATE: 26-Nov-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;
INFORMATION FOR SEQ ID NO: 16:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1208 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    FEATURE:
        NAME/KEY: Coding Sequence
        LOCATION: 1..651
;
US-09-517-849-16
        SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Alignment Scores:
Pred. No.:
Score: 1.34e-86
Percent Similarity: 1170.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-09-517-849-16

US-09-976-740-7 (1-217) x US-09-517-849-16 (1-1208)

Qy   1 GluGluArgValLeuGluLysGlyGluGluGluGluAspAspAspAspGluGluAspGluGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAA 60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACCAGCTTAACGGCGGAGCGCGGGACCTCAGAGTCGCCAAGGAGAGGGTCAAGGAGTGGACC 180

Qy   61 ProCysGlyProHisGlnHisGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCGGCCCCGGGCAGCGGCCACC 240

RESULT 3

US-09-616-289-16

Sequence 16, Application US/0961628 9

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)

SOFTWARE: FastSEQ for Windows Version 4.0

Alignment Scores:

Pred. No.:
Score: 1170.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:

Length: 1208
Matches: 217
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

1.34e-86
4

US-09-976-740-7 (1-217) x US-09-616-289-16 (1-1208)

```
Qy   1 GluGluArgValLeuLysGluGluGluGluLysLysAspAspAspGluAspGluGluGlu 20
Db   1 GAAGAGCGAGTACTTGAAGAAGAAGAAGAAGAAGATGATGATGAAGATGAAGATGAAGAA 60

Qy  21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
Db  61 GATGAAGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 120

Qy  41 HisGlnLeuAsnGlyLeuArgGlyProGlnSerIleAlaLysGluArgValLysGluTrpThr 60
Db 121 CACCAGCTTAACGGCGAGCGGGGGACCTCAGAGTCATCGCAGAGTGTGAAGGAGTGGACC 180

Qy  61 ProCysGlyProHisGlnGlyGlnAspGlyGlyAlaProGlyAlaProGlySerGlyThr 80
Db 181 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGGCGGCCCGGGGCACCCGGGAGTGGCAC 240

Qy  81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
Db 241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCGGTTGCCACC 300

Qy 101 GlyProCysAspSerProSerProValProLeuProLeuProLeuProGlyAla 120
Db 301 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCTGCCCTTACCTGGGGGC 360

Qy 121 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
Db 361 GACGGGACCCCTTTGGCGTGTCCTCCTGGCGAAAGGAGAAGCCATCTGATCCCGTCGAG 420

Qy 141 TrpThrValMetAspValValGlnThrTyrPheThrGluAlaGlyGlyProGluGlnAlaThr 160
Db 421 TGGACACGGTGATGGAAGTGGTCCAGACATATTTTACTGAGGCTGGAGGCCCGGAGCAGGCGACA 480

Qy 161 AlaPheGlnGluGlnGlnIleAspSerGlyLysSerSerLeuLeuLeuMetGlnAlaArgThrAspVal 180
Db 481 GCTTTCCAAGAGCAGCAGAAAATTGATGGCAAAATCTTTGCTCGTGTTGTTGCCACC 540

Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeu 200
Db 541 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG 600

Qy 201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db 601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGGATGGCTTCTTAGGC 651
```

RESULT 4

US-09-616-289-45

Sequence 45, Application US/0961628 9

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

```
Qy   1 GluGluArgValLeuLysGluGluGluGluLysLysAspAspAspGluAspGluGluGlu 20
```

```
;  NAME/KEY: CDS
;  LOCATION: (1)...(1614)
US-09-616-289-45

Alignment Scores:
Pred. No.:              1.94e-86
Score:                  1170.00        Length:         1614
Percent Similarity:     100.00%        Matches:        217
Percent Identity:       100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            4               Indels:         0
DB:                                     Gaps:           0

US-09-976-740-7 (1-217) x US-09-616-289-45 (1-1614)

Qy    1 GluGluArgValLeuGluHisGluGluGluGluAspAspAspGluAspGluGlu 20
Db  964 GAAGAGCGAGTACTTGAGAAAGAAGAGAAGAAGAAGAGATGAATGATGAAGAA 1023

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
Db 1024 GATGATGTGTCAGAGGGCCTCGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCGCAGCAC 1083

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluThrTrpThr 60
Db 1084 CACCAGCTTAACGGCGAGCGCGGGACCTCAGAGTGCCAAGGAGAGTGGGAC 1143

Qy   61 ProCysGlyProHisGlnGlyGlnGlyValProGlyProAlaProGlySerGlyThr 80
Db 1144 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCCGGGGGCCAGCGGGCACC 1203

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 100
Db 1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGCGGAGGCACAGCTTCTGTTGCCACC 1263

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db 1264 GGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGC 1323

Qy  121 AspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAspProValGlu 140
Db 1324 GACGGGACACCCCTTTGGCTGTCCGCCCGGCCGCAAAAGAAGCCATCTGATCCCGTCGAG 1383

Qy  141 TrpThrValMetAspValValGluThrTyrPheThrGluIleAspGlyPheProGlnGlnAlaThr 160
Db 1384 TGGACCGTGATGGACGTCGTCGAAATATTTACTGAGGGTCTGGATTTCCCGCAGCAGGCGACA 1443

Qy  161 AlaPheGlnGluGlnIleLeuAspGlyLysSerIleLeuLeuLeuMetGlnArgThrAspVal 180
Db 1444 GCTTTCCAAGAGCAGAGGAAATTGATAGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG 1503

Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
Db 1504 CTCACCGGCCTGTCCATCCCGCCTCGGGCCCCAGCCCTGAAAATCTACGAGCACCACATCAAG 1563

Qy  201 ValLeuGlnGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db 1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGGATGGCTTCTTAGGC 1614
```

```
Alignment Scores:
Pred. No.:              1.45e-76
Score:                  1047.50        Length:         1362
Percent Similarity:     95.45%         Matches:        195
Percent Identity:       88.64%         Conservative:   15
Best Local Similarity:  89.53%         Mismatches:     7
Query Match:            4               Indels:         3
DB:                                     Gaps:           2

US-09-976-740-7 (1-217) x US-08-979-608A-12 (1-1362)

Qy    1 GluGluArgValLeuGluHisGluGluGluGluAspAspAspGluAspGluGlu 20
Db   37 GAGGAGCGAGTGCTTGAAAAGAAGAGAGGAGGAGGAGGACGAGGACGAGGAC 96

Qy   21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
Db   97 GACGACGACGTCGGTGTCCGAGGGCGCTTCGGAGGGTGCCCGAGAGCGGATGC 156

Qy   39 GlnHisHisGlnLeuAsn-----GlyGluArgGlyProGlnSerAlaLysGluThrArgValLys 57
Db  157 CAGCATCACCAGCTGAATGGCGGCGAGCGCGGCCCAAGAGGAGGAGCCCAAG 216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnGlyValProGlyProAlaProGly 77
Db  217 GAGTGGTCCGCTGTGTGGCCCCAACCCTGGCCCCAGCAGCGCGGCCGCGGC 276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSer 97
Db  277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGGGGTAAGGAGGCGGCCTCT 336

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProLeuProProGlyLysProAlaLeu 117
Db  337 TCGACCACGGGCCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCTC 396

Qy  118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgGlyLysProSerAsp 137
Db                                                        ... 
```

Alignment Scores:
Pred. No.:   1.45e-76   Length: 1362
Score: 1047.50   Matches: 195
Percent Similarity: 95.45%   Conservative: 15
Best Local Similarity: 88.64%   Mismatches: 7

US-09-517-849-12
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;   LOCATION: 1...696
;   NAME/KEY: Coding Sequence
; FEATURE:
;   TOPOLOGY: linear
;   STRANDEDNESS: single
;   TYPE: nucleic acid
;   LENGTH: 1362 base pairs
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 12:
;   TELEFAX: 617/542-8906
;   TELEPHONE: 617/542-5070
; TELECOMMUNICATION INFORMATION:
;   REFERENCE/DOCKET NUMBER: 10797-003001
;   REGISTRATION NUMBER: 35,965
;   NAME: Myers, Louis
; ATTORNEY/AGENT INFORMATION:
;   FILING DATE: 26-NOV-1997
;   APPLICATION NUMBER: 08/979,608
; PRIOR APPLICATION DATA:
;   FILING DATE: 02-Mar-2000
;   APPLICATION NUMBER: US/09/517,849
; CURRENT APPLICATION DATA:
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   OPERATING SYSTEM: DOS
;   COMPUTER: IBM Compatible
;   MEDIUM TYPE: Diskette
; COMPUTER READABLE FORM:
;   ZIP: 02110-2804
;   COUNTRY: USA
;   STATE: MA
;   CITY: Boston
;   STREET: 225 Franklin Street
;   ADDRESSEE: Fish & Richardson P.C.
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 42
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   Arjona, Anibal A.
;   Law, Simon W.
;   Lees, Robert S.
; APPLICANT: Lees, Ann M.
; GENERAL INFORMATION:
; Patent No. 6605588
; Sequence 12, Application US/09517849
; US-09-517-849-12
RESULT 6

Qy 397 CCAGGAGCCGGATGGGAGCCCCCTTTGGCTGCCTGCCCTGGGGGCGGCCAAAGAGAAGCCGCGCAGAC 456
Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
Qy 457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGCGCGGGGGCTTCCTGAG 516
Qy 158 GlnAlaThrAlaPheGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 517 CAAGCCACACGGCGCTTTCCAGGAGGAGGATCGACACGGCCAAGTCCCTGCTGCTCATGCAGCGC 576
Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 577 ACCGGATGTCCTCACCGGCCCTGTCCATCCGCCTGGGCGCCGGTTGAAAAATCTATGAGCAC 636
Qy 198 HisIleLysValLeuGlnGlnGlyHisSerPheGluAspAspProAspGlyPheLeuGly 217
Db 637 CATATCAAGGTGCTGCAGCAGGTCACTTCGAGGACGATGACCCGAAGGCTTCCTGGGA 696

Query Match: 89.53%   Indels: 3
DB: 4   Gaps: 2

US-09-976-740-7 (1-217) x US-09-517-849-12 (1-1362)

Qy   1 GluGluArgValLeuGlyLysGluGluGluAspAspProGluGluGlu 20
Db   37 GAGGAGCGAGTGCTTGAAAAAGGAGGAGGAGGAGGAGGACGAGGACGAC 96

Qy   21 AspAsp------ValSerGluGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
Db   97 GACGACGACGAGCTCGTGTCCGAGGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCGGCCGGGTGCG 156

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyTyrGlnSerAlaLysGluArgValLys 57
Db 157 CAGCATCACCAGCTGAAATGGCGCGGGAGCGGGGTACCAGAGCGCCAAAGAGCGGGTGAAG 216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyProGlnGlnAspGluGlyIleArgGlyProAlaProGly 77
Db 217 GAGTGGTCGCCGTGTGGTCCGCACCAGGGCCCAGCAGGACGAGGGGATCCGGGGCCCGGCGCCCGGC 276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSer 97
Db 277 AGTGGCACCCGCCAGGTGTTCTCATGGCGGCGATGAACAAGGAGGGGGGATCAGCCTCT 336

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyGlyGlyProAlaLeu 117
Db 337 TCGACCACCGGACCCGACTCCCCGTCTCCCGTGCCTTTGCCCCCGGGAGGGGGAGGCCCCCTC 396

Qy 118 ProGlyAlaAspGlyThrProHisPheGlyCysProProGlyTyrArgGlyLysProSerAsp 137
Db 397 CCAGGAGCCGGATGGGACCCCCCATTTGGCTGCCCCCGGGCTACAGAGGGAAGCCGAGCGAC 456

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
Db 457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG 516

Qy 158 GlnAlaThrAlaPheGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 517 CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC 576

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 577 ACCGGATGTCCTCACCGGCCCTGTCCATCCGCCTGGGCGCCGGTTGAAAAATCTATGAGCAC 636

Qy 198 HisIleLysValLeuGlnGlnGlyHisSerPheGluAspAspProAspGlyPheLeuGly 217
Db 637 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGAAGGCTTCCTGGGA 696

RESULT 7
US-09-616-289-12
; Sequence 12, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   APPLICANT: Lees, Robert S.
;   APPLICANT: Law, Simon W
;   APPLICANT: Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;   TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;   TITLE OF INVENTION: ATHEROSCLEROSIS
;   FILE REFERENCE: 10797-004001
;   CURRENT APPLICATION NUMBER: US/09/616,289
;   CURRENT FILING DATE: 2000-07-14
;   PRIOR APPLICATION NUMBER: US 09/517,849
;   PRIOR FILING DATE: 2000-03-02
;   PRIOR APPLICATION NUMBER: US 08/979,608
;   PRIOR FILING DATE: 1997-11-26
;   PRIOR APPLICATION NUMBER: US 60/031,930
;   PRIOR FILING DATE: 1996-11-27
;   PRIOR APPLICATION NUMBER: US 60/048,547
;   PRIOR FILING DATE: 1997-06-03
;   NUMBER OF SEQ ID NOS: 53

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(696)
; US-09-616-289-12
```

Alignment Scores:

```
Pred. No.:
Score:                    1.45e-76        Length:        1362
Percent Similarity:       1047.50         Matches:       195
Best Local Similarity:    95.45%          Conservative:  15
Query Match:              88.64%          Mismatches:    7
DB:                       89.53%          Indels:        3
                          4               Gaps:          2
```

US-09-976-740-7 (1-217) x US-09-616-289-12 (1-1362)

```
Qy      1  GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluGlu  20
           |||||||||||||||||||||||::|||:||||||||||||||||||||||||||
Db     37  GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAAGAGGACGACGAGGACGAC  96

Qy     21  AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla  38
           |||||       ||||||||||||||||||||||||||||||||||||||||||||||||
Db     97  GACGACGAGGTGTCTGAGGGCTCCGAGGTCCCGGAGAGCGATCGTCCCGGCGGGCGGGTGCG  156

Qy     39  GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgGlyValLys  57
           |||::||||||||||:      |||:|||||||||||||:|||||:||||||||||||||| |||
Db    157  CAGCATCACCAGCTGAATGGCGGCGGCGGCCCGCAGAGCGCCAAGGAGCGCGGGGCCAAG  216

Qy     58  GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly  77
           |||||||||||||||||||:||:|||||:|||:|||||||||||||:|||||||||  |||
Db    217  GAGTGGACGCCGTGTGGTCCCCACCCTGGCCCCAGGAGGAGGGGCGGGGCCGGGC  276

Qy     78  SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer  97
           ||||||||||||||||||:||:||||||||||::|||||||||:|:||||||||:||||||
Db    277  AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGGAGGGGGGATCAGCCTCT  336

Qy     98  ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu  117
           |||||||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||
Db    337  TCGACCACCGGGCCGGACTCCCCGTCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTC  396

Qy    118  ProGlyValAspSerGlyThrProPheGlyCysProProGlyArgLysGlyProSerSerAsp  137
           |||||||||:||||:|||||||||||:|||||||||||:||||||||||||:|||::|||
Db    397  CCAGGAGGCCGATGGGACCCCCTTTGGCTGCCCGCCGGGGCGGAAGGGCCCGGCCAGC  456

Qy    138  ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu  157
           |||::|||||||||:|||:||||||||:||||||||||||:|||||||||||||||||||:
Db    457  CCCGTGGAGTGGACAGTCATGGACGTCGTTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG  516

Qy    158  GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg  177
           ||||||||||:||||||||||||||:||||||||||||:||||||||||||||||:|||:|||
Db    517  CAAGCCACGGCCTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC  576

Qy    178  ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis  197
           ||||||||||||||||||||||:||:|||||||||||||||:|||||||||||||||||
Db    577  ACCGACGTCCTCACCGGCCTCTCCATCCGGCTGGGCCCGGCGTTGAAAATCTATGAGCAC  636

Qy    198  HisIleLysValLeuGlnIleGlnHisPheGluAspAspAspProAspGlyPheLeuGly  217
           ||||||:|||:||||:|||||:|:|:|||||||:|:||::|||||:|||||:||||:|||
Db    637  CATATCAAGGTGCTGCAGCAGGGTCACTTCCAGGAGGACGATGACCCGGACGGCTTCCTGGGA  696
```

RESULT 9
US-09-517-849-13
Sequence 13, Application US/0951849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
 Lees, Robert S.
 Law, Simon W.
 Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/517,849
 FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/979,608
 FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis
 REGISTRATION NUMBER: 35,965
 REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
 LENGTH: 1422 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...756
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-517-849-13

```
Qy    98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 TCGACCACCGGGCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCCGGGAAGCCCGCCCTC 456

Qy   118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAsp 137
         |||||||||||||:|||:|||||||||||||||||||||||||||||||||:||||||
Db   457 CCAGGAGCCGGATGGGAGACCCCCTTTGGCTGCCCCTGCCCAAAGAGAGCCCGGCAGAC 516

Qy   138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluIleAlaGlyProGlu 157
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517 CCCGTGGAGTGGACAGTGATGGACGTCGTGGAGTACTTCACGGAGATCGCGGGCCTTGAG 576

Qy   158 GlnAlaThrAlaPheGlnValGlnValIleAspGlyGlyLysSerLeuLeuLeuMetGlnArg 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577 CAAGCCACGGCGTTTCCAGGAGACCAGGAGATCGACGGCGGAAGTCCCTGCTGCTCATGCAGCGC 636

Qy   178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   637 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCCGCCCTGAAAATCTATGAGCAC 696

Qy   198 HisIleLysValLeuGlnIleGlyHisPheGluAspAspProAspGlyPheLeuGly 217
         ||||||||||||||||||||||||||:||:|||||:||||||||||:|||||||||
Db   697 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGACGGAAGGCTTCCTGGGA 756
```

Alignment Scores:
Pred. No.:
Score: 1.53e-76 Length: 1422
Percent Similarity: 1047.50 Matches: 195
Best Local Similarity: 95.45% Conservative: 15
Query Match: 88.64% Mismatches: 7
DB: 89.53% Indels: 3
        4   Gaps: 2

US-09-976-740-7 (1-217) x US-09-517-849-13 (1-1422)

```
Qy     1 GluGlyArgValLeuGluGlyLysGluGluGlnGluAspAspGluGlu 20
         |:|||||||||:|:|||||||||:|||::::::||
Db    97 GAGGAGAGCGAGTGGCTTGAAAAAGGAGGAGGAGGAGGAGAAGACGACGAGGAGACGAC 156

Qy    21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
         ||||||:||||||||||||||||||||||||||||||||:|||||||
Db   157 GACGACGACGATGGTTCGGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCGGCGGGTGCG 216

Qy    39 GlnHisHisGlnLeuAsn---GlyGluArgGlyTyrProGlnSerAlaLysGluArgValLys 57
         |||||:||||||||||:|||||||||||||:||||||||||||:|||||
Db   217 CAGCATCACCAGCTGAATGGCGGCGGGGAGCGCGGCTACCCGCAGTCGGCCAAGGAGCGGGTCAAG 276

Qy    58 GluTrpThrProCysGlyProHisGlnGlyHisGlnAspGluLysGlyArgGlyProAlaProGly 77
         ||:||||||||:|||||:||||||||:|||||||||||||||:|||||||||||||||:|||||
Db   277 GAGTGGTCGCTGTGTGGCCCCCACCCTGGCCAGGAGGAGGGGGGCGGGGCCGGGCGCCGGGC 336

Qy    78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
         ||||||||||||||||||||||||||||||||||||:|||:|||||:||:|
Db   337 AGTTGGCACCGCCCAGGTGTTCTCCATGGCCGCCATGAATAAGGAGGGGGGGATCAGCCTCT 396

Qy    98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 TCGACCACCGGGCCTGACTCCCCGTCCCCGGTGCCTTTGCCCCCCGGGAAGCCCGCCAGAC 456

Qy   118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAsp 137
         |||||||||||:|||:|||||||||||||||||||||||||||||||:|||||||
Db   457 CCAGGAGCCGGATGGGACCCCCTTTGGCTGCCCCTGCCCAAAGAGAGCCCGGCAGAC 516

Qy   138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluIleAlaGlyProGlu 157
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACGGAGATCGCGGGCCTTGAG 576

Qy   158 GlnAlaThrAlaPheGlnValGlnValIleAspGlyGlyLysSerLeuLeuLeuMetGlnArg 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577 CAAGCCACGGCGTTTCCAGGACCAGGAGATCGACGGCGGAAGTCCCTGCTGCTCATGCAGCGC 636

Qy   178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   637 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCCGCCCTGAAAATCTATGAGCAC 696

Qy   198 HisIleLysValLeuGlnIleGlyHisPheGluAspAspProAspGlyPheLeuGly 217
         ||||||||||||||||||||:||:|||||:|||||||||||||:|||||||||
Db   697 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGACGGAAGGCTTCCTGGGA 756
```

RESULT 10
US-09-616-289-13
Sequence 13, Application US/0916289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608

```
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
;  LENGTH: 1422
;  TYPE: DNA
;  ORGANISM: Oryctolagus cuniculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(756)
US-09-616-289-13

;  DB:
Query Match:
Best Local Similarity:
Percent Similarity:
Score:
Pred. No.:
Alignment Scores:
```

US-09-976-740-7 (1-217) x US-09-616-289-13 (1-1422)

```
Length:        1422
Matches:        195
Conservative:    15
Mismatches:       7
Indels:           3
Gaps:             2
```

```
Qy    1 GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||||||||||:::||||:||:::
Db   97 GAGGAGCGAGTGCTTGAAAAAGGAGGAGGAGGAGGAAGACGACGAGGACGAC 156

Qy   21 AspAsp-------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
         |||||       ||||||||||||||||||||||:::||||||||||||||||||||||
Db  157 GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGGTGCG 216

Qy   39 GlnHisHisGlnLeuAsn-----GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
         ||||||||||||||||||     |||||||||:::||||||||||||||||||||
Db  217 CAGCATCACCAGCTGAATGGCGGCGACCCGCAAGGAAGCCGGGCCAAG 276

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyArgGlyProAlaProGly 77
         |||||||||||||||||||:::|||||||||||||||||||||||||||||
Db  277 GAGTGGTCGCTGTGTGGCCCCACCCTGGCCAGGAGGAGAAGGGCGGGGCCGGGGGC 336

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
         ||||||||:::||||||||||||||||||:::||||||||||||||||
Db  337 AGTGGCACCCGCCAGGTGTTCTCATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCTCT 396

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  397 TCGACACCAGGGCCTGACTCCCCGTCCCCCGGTTGCCCCTCCCCCGGAAGCCAGCCCTC 456

Qy  118 ProGlyAlaAspGlyThrProHisGlyCysSerProProGlyArgGlyLysProSerAsp 137
         ||||||:::||||||||||||||||||||||||||||||||||||:::|||
Db  457 CCAGGAGCCGATGGGACACCCCTTGGCCTGCGCCCGGGCGCCAAAGAGAACCCGGCAGAC 516

Qy  138 ProValGlyTrpThrValMetAspValValGlyTyrPheThrArgGluIleGlyPheProGlu 157
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  517 CCCGTGGGATGGACAGTCATGGACGTCGTGGGGTACTTCACCGAGGGGGCTTCCCTGAG 576

Qy  158 GlnAlaThrAlaPheGlnGlnLeuGlnLeuAspGlyLysSerLeuLeuLeuMetGlnArg 177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  577 CAAGCCACGGCTTTCCAGGAGCAGGAGCTGCAGGATGGACGGAAGTCCCTGCTGCTCATGCAGCGC 636

Qy  178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
         |||||:::||||||||||||||||||||||||||||||||||||||||
Db  637 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGCCCAGCGTTGAAAATCTATGAGCAC 696

Qy  198 HisIleLysValLeuGlnGlyHisProGluAspAspProAspGlyPheLeuGly 217
         |||:::|||||||||||||||||||||||||||||||||||||:::|||
Db  697 CATATCAAAGTGCTCGAGCAGGGTCACTTCGAGGACGACCCGGACGGGCTTCCTGGGA 756
```

Patent No. 6355451

```
;  GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;            Law, Simon W.
;            Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;       TREATING ATHEROSCLEROSIS
;  NUMBER OF SEQUENCES: 42
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Fish & Richardson P.C.
;  STREET: 225 Franklin Street
;  CITY: Boston
;  STATE: MA
;  COUNTRY: USA
;  ZIP: 02110-2804
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette
;  COMPUTER: IBM Compatible
;  OPERATING SYSTEM: DOS
;  SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/979,608A
;  FILING DATE: 26-No. 6355451-1997
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 60/048,547
;  FILING DATE: 03-JUN-1997
;  APPLICATION NUMBER: US 60/031,930
;  FILING DATE: 27-NOV-1996
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Myers, Louis
;  REGISTRATION NUMBER: 35,965
;  REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 617/542-5070
;  TELEFAX: 617/542-8906
;  INFORMATION FOR SEQ ID NO: 11:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 1617 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-979-608A-11
```

```
;  DB:
Query Match:
Best Local Similarity:
Percent Similarity:
Score:
Pred. No.:
Alignment Scores:
```

US-09-976-740-7 (1-217) x US-08-979-608A-11 (1-1617)

```
Length:        1617
Matches:        195
Conservative:    15
Mismatches:       7
Indels:           3
Gaps:             2
```

```
Qy    1 GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||||||||||:::||||:||:::
Db  292 GAGGAGCGAGTGCTTGAAAAAGGAGGAGGAGGAGGAAGACGACGAGGACGAC 351

Qy   21 AspAsp-------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
         |||||       ||||||||||||||||||||||:::||||||||||||||||||||||
Db  352 GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGGTGCG 411

Qy   39 GlnHisHisGlnLeuAsn-----GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
         ||||||||||||||||||     |||||||||:::||||||||||||||||||||
Db  412 CAGCATCACCAGCTGAATGGCGGCGACCCGCAAGGAAGCCGGGCCAAG 471

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyArgGlyProAlaProGly 77
         |||||||||||||||||||:::|||||||||||||||||||||||||||||
Db  472 GAGTGGTCGCTGTGTGGCCCCACCCTGGCCAGGAGGAGAAGGGCGGGGCCGGGGGC 531

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
```

Left column

```
Db 532 AGTGGCACCCCGCCAGGTGTTCTCCANGGCGGCGGCCCTTGAGTAAGGAGGGGGGGATCAGCCTCT 591
Qy  98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
Db 592 TCGACCACCGGGCGCTGACTCCCCGTCCCCGTGCCTTTGCCCCCCGGAAGCCAGCCCTC 651
Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyAlaArgLysGlyLysProSerAsp 137
Db 652 CCAGGAGCCGGATGGGACCCCCTTTGGCTGCCGGGCCCAAAGAGAAGCCGGCAGAC 711
Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
Db 712 CCCGTGGAGTGGACAGTCATGGACGTGGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG 771
Qy 158 GlnAlaThrAlaPheGlnGlnGluGlnIleIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 772 CAAGCCACGGCTTTCCAGGAGCAGGAGATCAACGGGAAGTCCCTGCTCCTGATGCAGCGC 831
Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 832 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCCGCCCTGAAAATCTATGAGCAC 891
Qy 198 HisIleLysValLeuGlnGlyIleHisPheGluAspAspAspGlyPheLeuGly 217
Db 892 CATATCAAGGTGCTGCAGGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGGA 951
```

RESULT 12
US-09-517-849-11
Sequence 11, Application US/0951849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Right column

Alignment Scores:

Pred. No.:	1.8le-76	Length:	1617
Score:	1047.50	Matches:	195
Percent Similarity:	95.45%	Conservative:	15
Best Local Similarity:	88.64%	Mismatches:	7
Query Match:	89.53%	Indels:	3
DB:	4	Gaps:	2

US-09-976-740-7 (1-217) x US-09-517-849-11 (1-1617)

```
Qy   1 GluGlyLeuArgValLeuGlyLysGluGlyGluGluAspAlaAspGluAspGluGlu 20
Db 292 GAGGGACCGAGTGGTTGCTTGAAAAAGGAGGAGGAGGAGGAGGACGACGAGGAGGAC 351
Qy  21 AspAsp------ValSerGluGlyGluValProGluSerSerAspAlaGlyLysAla 38
Db 352 GACGACGACGACTTCGTGTCTCCGGAGGGTGCCCGAGAGTCGTCCCGGGTGGGTGCG 411
Qy  39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysValIleArgValLys 57
Db 412 CAGCACCACCAGCTGAATGCGGGCGAGCGCGGCCCGCAGTCGGCCAAGGTGATCCGCGTGAAG 471
Qy  58 GluTrpThrProCysGlyProHisGlnGlnGlnGlyGlnAspGlyAspGlyGlyProAlaProGly 77
Db 472 GAGTGGACGCCGTGCGGTCCCCACCAGCTGGCCAGGAGCGAGGGCGGGGGGCCCGGGC 531
Qy  78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
Db 532 AGTGGCACCCCGCCAGGTGTTCTCCATGGGCGGCGGCCCTTGAGTAAGGAGGGGGGGATCAGCCTCT 591
Qy  98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
Db 592 TCGACCACCGGGCGCTGACTCCCCGTCCCCGTGCCTTTGCCCCCCGGAAGCCAGCCCTC 651
Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyAlaArgLysGlyLysProSerAsp 137
Db 652 CCAGGAGCCGGATGGGACCCCCTTTGGCTGCCGGGCCCAAAGAGAAGCCGGCAGAC 711
Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
Db 712 CCCGTGGAGTGGACAGTCATGGACGTGGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG 771
Qy 158 GlnAlaThrAlaPheGlnGlnGluGlnIleIleAspGlyLysSerLeuLeuLeuMetGlnArg 177
Db 772 CAAGCCACGGCTTTCCAGGAGCAGGAGATCAACGGGAAGTCCCTGCTCCTGATGCAGCGC 831
Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 832 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCCGCCCTGAAAATCTATGAGCAC 891
Qy 198 HisIleLysValLeuGlnGlyIleHisPheGluAspAspAspGlyPheLeuGly 217
Db 892 CATATCAAGGTGCTGCAGGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGGA 951
```

RESULT 13
US-09-616-289-11
Sequence 11, Application US/0961628 9
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(951)
US-09-616-289-11

```
Alignment Scores:
Pred. No.:                          1.81e-76     Length:        1617
Score:                              1047.50      Matches:        195
Percent Similarity:                 95.45%       Conservative:    15
Best Local Similarity:              88.64%       Mismatches:       7
Query Match:                        89.53%       Indels:           3
DB:                                 4            Gaps:             2
```

US-09-976-740-7 (1-217) x US-09-616-289-11 (1-1617)

```
Qy   1 GluGluArgValLeuGluLysGluLysGluGluGluGluGluAspAspAspGluAspGluGlu 20
        |||||||||||||||||||||||||||||||||:|||:||||:::||:::
Db 292 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAAGACGACGAGGAGGAC 351

Qy  21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
        |:::       |||||||||||||||||||||||||||||||:|||||||
Db 352 GACGACGAGACTCGTGTCCGAGGGTGCCGAGAGCGATCGTCCCGGGTGCG 411

Qy  39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
        ||||||||||||||||     ||||||||||||||||||||||||||||||
Db 412 CAGCACCACCAGCTGAATGGCGAGCGCGGCCCGCAGAGCGCGAAGGAGCGCGGCCAAG 471

Qy  58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly 77
        |||||||||||||||||:::||||||||||||:||||||||||||||||||
Db 472 GAGTGGACGCCGTGTGGCCCCCACCAGGGACAGGACGAGGGCCGCGGCCCCGCGCCCGGC 531

Qy  78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
        ||||||||||||||||||||||||||||||||||||:|||||||:::||||
Db 532 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGTCGGGATCAGCCTCT 591

Qy  98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 592 TCGACCACCGGCCCTGACTCCCCGTCCCCGGTCCCCCCGGGAAGCCAGCCCTC 651

Qy 118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAsp 137
        |||||||||||||||||||||||||||||||||||||||||:::|||||
Db 652 CCAGGAGCCGATGGACCCCCTTGGCTGCCCCCCAAAGAGAAAGGGATCGCCAGAC 711

Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
        |||||||||||||:||||||||||||||||||||||||||||||||||||
Db 712 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCCGGCTTCCCTGAG 771

Qy 158 GlnAlaThrAlaPheGlnIleGlnLeuIleAspGlyLysLysSerLeuLeuMetGlnArg 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 772 CAAGCCACGGCTTTCCAGGAGCAGGAGAATCGGTTGAAAAATCTATGAGCAGCAC 831

Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 832 ACCGATGTCCTCACCGGCCTGAGCATCCGGCTGGGGCCAGCGTTGAAAATCTATGAGCAC 891

Qy 198 HisIleLysValLeuGlnIleGlyHisGlnAspAspAspGlyPheLeuGly 217
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 892 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGGATGACCCCGAAAGGCTTCCTGGGA 951
```

; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-09-616-289-48

```
Alignment Scores:
Pred. No.:                          3.23e-76     Length:        2561
Score:                              1047.50      Matches:        195
Percent Similarity:                 95.45%       Conservative:    15
Best Local Similarity:              88.64%       Mismatches:       7
Query Match:                        89.53%       Indels:           3
DB:                                 4            Gaps:             2
```

US-09-976-740-7 (1-217) x US-09-616-289-48 (1-2561)

```
Qy    1 GluGluArgValLeuGluLysGluLysGluGluGluGluGluAspAspAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||:|||:||||:::||:::
Db 1236 GAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAAGACGACGAGGAGGAC 1295

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
         |:::       |||||||||||||||||||||||||||||||:|||||||
Db 1296 GACGACGAGACTCGTGTCCGAGGGTGCCGAGAGCGATCGTCCCGGGTGCG 1355

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys 57
         ||||||||||||||||     ||||||||||||||||||||||||||||||
Db 1356 CAGCATCACCAGCTGAATGGCGAGCGCGGCCCGCAGAGCGCGAAGGAGCGCGGCCAAG 1415

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly 77
         |||||||||||||||||:::||||||||||||:||||||||||||||||||
Db 1416 GAGTGGACGCCGTGTGGCCCCCACCAGGGACAGGACGAGGGCCGCGGCCCCGCGCCCGGC 1475

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
         ||||||||||||||||||||||||||||||||||||:|||||||:::||||
Db 1476 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAACAAGTCGGGATCAGCCTCT 1535

Qy   98 ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1536 TCGACCACCGGCCCTGACTCCCCGTCCCCGGTCCCCCCGGGAAGCCAGCCCTC 1595

Qy  118 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAsp 137
         |||||||||||||||||||||||||||||||||||||||||:::|||||
Db 1596 CCAGGAGCCGATGGACCCCCTTGGCTGCCCCCCAAAGAGAAAGGGATCGCCAGAC 1655

Qy  138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
         |||||||||||||:||||||||||||||||||||||||||||||||||||
Db 1656 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCCGGCTTCCCTGAG 1715
```

RESULT 14
US-09-616-289-48
; Sequence 48, Application US/0961 6289

RESULT 15
US-09-616-289-50
; Sequence 50, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Arjona, Anibal A.
; APPLICANT: Law, Simon W.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-50

Alignment Scores:
Pred. No.:
Score: 1036.50
Percent Similarity: 69.01%
Best Local Similarity: 69.01%
Query Match: 88.59%
DB:

Length: 12425
Matches: 216
Conservative: 0
Mismatches: 1
Indels: 97
Gaps: 3

1.87e-74

US-09-976-740-7 (1-217) x US-09-616-289-50 (1-12425)

```
Qy    1 GluGluArgValLeuGluGlyLysGluGluGlyLuAspAlaSpGluAspGluGlu 20
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 4217 GAAGAGGCGGACTTGAGAAGAGAGGAAGAAGATGATGAAGATGAAGATGAAGAA 4276

Qy   21 AspAspValSerGlySerGlyValProLuSerAspArgProAlaGlyValAlaGlnHis 40
          ||||||||||||||||||||||||||||||||||||||||||||
Db 4277 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGGAGTGACCCGTCCTCCTGCCCAGGCAC 4336

Qy   41 HisGlnLeuAsnGlyIleuAspGluGlyArgGlyProGlnSerAlaLysGluGluTrpThr 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4337 CACCAGCTTAACGGCGGAGGGGAACCCTCAGGACGTGCCAAGGAGGAGTGGACC 4396

Qy   61 ProCysGlyProHisGlnGlyArgGlyArgGlyProCysAlaProGlySerGlyThr 80
          |||||||||||||||||||||||||||||||||||||||||||
Db 4397 CCCTGCGGGCCACCGCACCAGGGGCGAGGGGGCCGGGGCCGCGGCACC 4456

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysSerGluGlyGlyThr------------ 95
          ||||||||||||||||||||||||||||||||||||
Db 4457 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGAGTGAAGGAGGGTAGGATCCCTCT 4516
```

```
Qy   95 ---------------------------------------------------------- 95
Db 4517 GGGTGGGGAAGAGTGCTAGGTGGGAGGAGGAACTCAGCGTCCGAAGACAAAAGCCAAAGACAGGT 4576

Qy   96 --------AlaSerValAlaThrGlyProAspSerProSerProValProIle 110
                  ||||||||||||||||||||||||||||
Db 4577 GTTTTTTTCCTTCCCAGCTTCTGTTGCCACGGGACTCCCCGTCCCCGTGCCTTT 4636

Qy  110 uProProGlyLysProAlaLeuProGlyAlaAlaSpGlyThrProProPheGlyCysPro----- 128
          |||||||||||||||||||||||   :::||||||||||
Db 4637 GCCCCCAGGGAAACCAGCCCTACCTGGGGGCCGGACCCCCTTGGCGTGTCCCTAAGT 4696

Qy  128 ------------------------------------------------------------- 128
Db 4697 TGGGGGTATTGGAGACATGGGGGGTGCTTCAGGGGTGTGGGTACAGCGAGAGACATCCG 4756

Qy  129 ------------------------------------ProGlyArgGlysGluLysProSerAsp 138
                                              |||||||||||
Db 4757 TGTTCACTGGTGTCTCGTTTGTTTGATGCAGTCCCGGGGCGGCCAAACGAGAACCATCTGATC 4816

Qy  138 roValGluTrpThrValMetAspValAlaGluTyrPheThrGluAlaGlyPheProGluG 158
          |||||||||||||||||||||||||||||||||||||||||||
Db 4817 CCGTCCAGTGGACCCGTGATGGATGCGTCGTCAAATATTTTACTGAGGCTGGAATTCCGGAGC 4876

Qy  158 lnAlaThrAlaPheGlnGlu-------------------------------------- 164
          ||||||||||||||||
Db 4877 AGGCGACAGCTTTCCAAGA-GCAGTGAGTTTCAGCCCCAGGACTACACACTGACGAGACA 4935

Qy  165 ----------------------------------------------------GlnG 166
                                                              ||||
Db 4936 CAGAGGGCGCTCCCTGGGGATGCCCGATCCCGGCGTTTCTTCGTCGTTCCCACCCAGG 4995

Qy  166 lullleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerI 186
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 4996 AAATTGATGCGCAAATCTTTGCTGCTCATGCAGCGGACAGAGTGCTCACCGGGCCTGTCCA 5055

Qy  186 leArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnIleGlyH 206
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 5056 TCCGCCTGGGGCCAGCGCTGAAAAAATCTACGAGCACCACATCAAGGTGCTCAGCAAGGCC 5115

Qy  206 isPheGluLeuAspAspAspAsnProAspGlyPheLeuGly 217
          |||||||||||||||||||||||||||||
Db 5116 ACTTCGAGGATGATGACCCCCGATGGCTTCTTAGGC 5150
```

```
Qy  158 GlnAlaThrAlaPheGlnGluGlnIleuAspGlyLysSerLeuLeuLeuMetGlnArg 177
          |||||||||||||||||||||||||||||||
Db 1716 CAAGCCACGGCGTTTCCAGGAGCAGGAGATCGACGGGCAAAGTCCCTGCTGCTCATGCAGCGC 1775

Qy  178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
          ||||||||||||||||||||||||||||||||
Db 1776 ACCGACGTCCTCACCGGCCTCTCCATCCGCCTGGGGCCAGCGTTGAAAATCTATGAGCAC 1835

Qy  198 HisIleLysValLeuGlnIleGlyHisPheGluLeuHisAspAspAsnProAspGlyPheLeuGly 217
          |||||||||||||||||||||||   :::|||||||||||
Db 1836 CATATCAAGGTGCTGCAGATCGGTCACTTCGAGGACGATGACCCGGACGGCTTCCTGGGA 1895
```

Search completed: March 13, 2004, 04:06:18
Job time : 82.5728 secs

```
                              GenCore version 5.1.6
                         Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:           March 12, 2004, 20:46:42 ; Search time 313.946 Seconds
                                             (without alignments)
                                             2544.725 Million cell updates/sec

Sequence:         US-09-976-740-7
Title:            1170
Perfect score:    1170
Sequence:         1 EERVLEKEEEEDDDEDEDEE.........HIKVLQQGHFEDDPDGFLG 217

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched:         2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters:     4865114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
  Published_Applications_NA:*
-MODE=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19588/app_query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DQCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0997674 @CGN_1_712 @runat_10032004_094549_19588
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        Published_Applications_NA:*
 1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 3:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 4:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 5:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 6:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 7:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 8:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result   Query    %      Match
No.      Score           Length   DB   ID        Description
------   -----   ---     ------   --   --------   -----------
```

ALIGNMENTS

```
RESULT 1
US-09-962-055-16
Sequence 16, Application US/09962055
Patent No. US20050052033A1
GENERAL INFORMATION:

  APPLICANT:  Lees, Ann M.
              Lees, Robert S.
              Law, Simon W.
              Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
              BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
              TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: Fish & Richardson P.C.
     STREET: 225 Franklin Street
     CITY: Boston
     STATE: MA
     COUNTRY: USA
     ZIP: 02110-2804
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Diskette
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: DOS
```

```
 1  1170   100.0   1208    9  US-09-962-055-16    Sequence 16, Appl
 2  1170   100.0   1208    9  US-09-976-740-16    Sequence 16, Appl
 3  1170   100.0   1208   12  US-10-671-242-16    Sequence 16, Appl
 4  1170   100.0   1208   13  US-10-023-523-16    Sequence 16, Appl
 5  1170   100.0   1208   13  US-10-023-529-16    Sequence 16, Appl
 6  1170   100.0   1208   15  US-10-616-187-16    Sequence 16, Appl
 7  1170   100.0   1445   10  US-09-945-527-6     Sequence 6, Appl
 8  1170   100.0   1614    9  US-09-976-740-45    Sequence 45, Appl
 9  1170   100.0   1614   12  US-10-671-242-45    Sequence 45, Appl
10  1170   100.0   1614   13  US-10-023-523-45    Sequence 45, Appl
11  1170   100.0   1614   13  US-10-023-529-45    Sequence 45, Appl
12  1170   100.0   1614   15  US-10-616-187-45    Sequence 45, Appl
13  1161    99.2   1336   14  US-09-962-055-247   Sequence 247, App
14  1047.5   89.5   1362    9  US-09-962-055-12    Sequence 12, Appl
15  1047.5   89.5   1362    9  US-09-976-740-12    Sequence 12, Appl
16  1047.5   89.5   1362   13  US-10-023-529-12    Sequence 12, Appl
17  1047.5   89.5   1362   13  US-10-023-523-12    Sequence 12, Appl
18  1047.5   89.5   1362   15  US-10-616-187-12    Sequence 12, Appl
19  1047.5   89.5   1362   15  US-10-616-187-12    Sequence 12, Appl
20  1047.5   89.5   1422    9  US-09-976-740-13    Sequence 13, Appl
21  1047.5   89.5   1422   12  US-10-671-242-13    Sequence 13, Appl
22  1047.5   89.5   1422   13  US-10-023-529-13    Sequence 13, Appl
23  1047.5   89.5   1422   13  US-10-023-523-13    Sequence 13, Appl
24  1047.5   89.5   1422   15  US-10-616-187-13    Sequence 13, Appl
25  1047.5   89.5   1422   15  US-10-616-187-13    Sequence 13, Appl
26  1047.5   89.5   1617    9  US-09-976-740-11    Sequence 11, Appl
27  1047.5   89.5   1617   12  US-10-671-242-11    Sequence 11, Appl
28  1047.5   89.5   1617   12  US-10-671-242-11    Sequence 11, Appl
29  1047.5   89.5   1617   13  US-10-023-529-11    Sequence 11, Appl
30  1047.5   89.5   1617   13  US-10-023-523-11    Sequence 11, Appl
31  1047.5   89.5   1617   15  US-10-616-187-11    Sequence 11, Appl
32  1047.5   89.5   2561    9  US-09-976-740-48    Sequence 48, Appl
33  1047.5   89.5   2561   12  US-10-671-242-48    Sequence 48, Appl
34  1047.5   89.5   2561   13  US-10-023-529-48    Sequence 48, Appl
35  1047.5   89.5   2561   13  US-10-023-523-48    Sequence 48, Appl
36  1047.5   89.5   2561   15  US-10-616-187-48    Sequence 48, Appl
37  1036.5   88.6  12425    9  US-09-976-740-50    Sequence 50, Appl
38  1036.5   88.6  12425   12  US-10-671-242-50    Sequence 50, Appl
39  1036.5   88.6  12425   13  US-10-023-529-50    Sequence 50, Appl
40  1036.5   88.6  12425   13  US-10-023-523-50    Sequence 50, Appl
41  1036.5   88.6  12425   15  US-10-094-749-1218  Sequence 1218, Ap
42  1036.5   88.6   1566   15  US-10-094-749-1218  Sequence 1218, Ap
43   300     25.6   1957   10  US-09-867-034-16    Sequence 16, Appl
44   285     24.4   1066   12  US-10-221-625-173   Sequence 173, App
45   285     24.4   1601   14  US-10-037-270-638   Sequence 638, App
```

Left column

SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-962-055-16

Alignment Scores:

Pred. No.:		Length:	1208
Score:	2.38e-99	Matches:	217
Percent Similarity:	1170.00	Conservative:	0
Percent Identity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	9		

US-09-962-055-16 (1-217) x US-09-976-740-7 (1-1208)

```
Qy    1 GluGluArgValLeuGluLysGluGluGluGluGluAspAspAspGluAspGluAspGluGlu   20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGCGAGTACTTGAGAAAGAGGAAGAAGATGATGATGAAGAGATGAAGATGAAGAA     60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis     40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC    120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGlyGluTrpThr             60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGCCAGCGCGGGACCTCAGAGTGCCAAGGAGGAGTGGACC          180

Qy   61 ProCysGlyProHisGlnGlyGlnArgGlyProAlaProGlySerGlyThr             80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCGCACCAGGGCCAGATGAAGGGCGGCGGGCCCCGGGCCAGGGCACC       240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyGlyThrAlaSerValAlaThr    100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGGAACAGCTTCGTTGCCACC    300

Qy  101 GlyProAspSerProSerProValProLeuProGlyProGlyAla                  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GGGCCAGACTCCCCGTCCCCGGTCCCTTTGCCCCGGCAAACCAGCCCTTACCTGGGGCC   360

Qy  121 AspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAspProValGlu    140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACGGGACCCCCTTTGGCTGTCCTCCCGGACGCAAAGAGAAGCCATCTGATCCCGTCGAG   420

Qy  141 TrpThrValMetAspValValGluTyrPheThrGluIleGlyPheProGluGlnAlaThr   160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TGGACCGTGATGGATGTCGTGGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA   480

Qy  161 AlaPheGlnGluGlnLeuAspGlyLysSerLeuLeuMetGlnArgThrAspVal          180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCTTTCCAAGAGCAGAGAAATTGATGGCAAATCTTGCTGCTCATGCAGCGCCACGATGTG   540
```

Right column

```
Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys    200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTCACCGGCCTGTCTCATCCGCCTCGGGCCGCCCTCAAGATCTACGAGCACCATCAAG     600

Qy  201 ValLeuGlnLeuGlyHisProAspAspAspGluAspGlyPheLeuGly               217
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGGCTTCTTAGGC          651
```

RESULT 2
US-09-976-740-16
Sequence 16, Application No. US09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)

US-09-976-740-16

Alignment Scores:

Pred. No.:		Length:	1208
Score:	2.38e-99	Matches:	217
Percent Similarity:	1170.00	Conservative:	0
Percent Identity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	9		

US-09-976-740-7 (1-217) x US-09-976-740-16 (1-1208)

```
Qy    1 GluGluArgValLeuGluLysGluGluGluGluGluAspAspAspGluAspGluAspGluGlu   20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGCGAGTACTTGAGAAAGAGGAAGAAGATGATGATGAAGAGATGAAGATGAAGAA     60

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis     40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC    120

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGlyGluTrpThr             60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGCCAGCGCGGGACCTCAGAGTGCCAAGGAGGAGTGGACC          180

Qy   61 ProCysGlyProHisGlnGlyGlnArgGlyProAlaProGlySerGlyThr             80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCGCACCAGGGCCAGATGAAGGGCGGCGGGCCCCGGGCCAGGGCACC       240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyGlyThrAlaSerValAlaThr    100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGGAACAGCTTCGTTGCCACC    300
```

Qy   101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCCAGACTCCCCGTCCCCGCTGCCTTTGCCCCCAGGCAAACCAGCCTTACCTGGGGCC 360

Qy   121 AspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAspProValGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGGGACACCCCCTTTGGCTGTCCTCCCGGGCCGCAAAGAGAAGCCAATCTGATCCCGG 420

Qy   141 TrpThrValMetAspValValGlyTyrPheThrGlnAlaGlyProGluGlnAlaThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGACCGTGATGGATGTCGTTGGGAATATTTACTGACGGCTGATTCCCGGAGGCAGGCGACA 480

Qy   161 AlaPheGlnGluGlnGluIleAlaAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTTTCCAAGAGCAGGAAATTGCATGGGGCTCCTGGAGGCTGGATTCCCGAGAGCAGGATGTG 540

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCAAAAATCTACGAGCACCACATCAAG 600

Qy   201 ValLeuGlnGlnGlnHisPheGluAspAspAspProAspGlyPheLeuGly 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGCTTCAGCAGAAGGCCCACTTTGAGGATGAGGATCCCGATGGCTTCTTAGGC 651

RESULT 3
US-10-671-242-16
Sequence 16, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-671-242-16

Alignment Scores:
Pred. No.:
Score: 2.38e-99
Percent Similarity: 1170.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:

Length: 1208
Matches: 217
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-7 (1-217) x US-10-671-242-16 (1-1208)

Qy   1 GluGluArgValLeuGlyLysGlyGlyLeuAspAspAspGlyAspAspGluGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGACGGAGTACTTGAGAAAGAAGAGGAAGAGGAAGATGATGATGAAGATGAAGAA 60

RESULT 4
US-10-023-529-16
Sequence 16, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/10/023,529
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Qy   21 AspAspValSerGluGlySerGluValValProGluSerArgProAlaGlyValAlaGlnHis 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTGTCAGAAGGCTCTGAAGTGGTCCCAGAGAGTGACCGCCCAGCTGGTGTGGCGCAGCAC 120

Qy   41 HisGlnLeuAsnGlyValArgGlyProGlnSerArgAlaLysGluArgValLysGluTrpThr 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACCAGCTTAACGGGGTGAGGGGACCTCAGAGTCGGGCGAAGGAGAGGGTGAAGGAGTGGACC 180

Qy   61 ProCysGlyProHisGlnGlyGlnAspGlyGlnGlyGlyGlyProAlaProGlySerGlyThr 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGCTGCGGCCCACACCAGGGCCAGGATGAGAAGGGCGGGGGACCAGCCCCAGGCTCAGGCACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CGCCAGGTGTTCTCCATGGCCGCCATGAACAAGGAGGGGACAGCTTCTGTTGCCACC 300

Qy   101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCTTACCTGGGGCC 360

Qy   121 AspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAspProValGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGGGACACCCCCTTTGGCTGTCCCCGGGCCGCAAAGGGAAGCCATCTGACCCCGG 420

Qy   141 TrpThrValMetAspValValGlyTyrPheThrGlnAlaGlyProGluGlnAlaThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGACCGTGATGGATGTCGTTGGAATATTTACTGAGGCTGGATTCCCGGAGGCAGGCGACA 480

Qy   161 AlaPheGlnGluGlnGluIleAlaAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTTTCCAAGAGCAGGAAATTGATGGCAAAATCTTTGCTCGTCATGCAGCGGCCACAGATGTG 540

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCAAAAATCTACGAGCACCACATCAAG 600

Qy   201 ValLeuGlnGlnGlnHisPheGluAspAspAspProAspGlyPheLeuGly 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGCTTCAGCAGAAGGCCCACTTTGAGGATGAGGATCCCGATGGCTTCTTAGGC 651

; NAME/KEY: CDS
; LOCATION: (1)....(651)
US-10-023-529-16

Alignment Scores:
Pred. No.:
Score: 2.38e-99   Length: 1208
                          1170.00   Matches: 217
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
                          13   Gaps: 0
DB:

US-09-976-740-7 (1-217) x US-10-023-529-16 (1-1208)

```
Qy    1  GluGlyArgValLeuGlyIleLysGluGluGluLeuAspAspAspGluAspGluGlu  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GAAGGACGAGTACTTGAGAAAAGAAGAAGAGAGAATGATGATGAAGATGAAGATGAAGAA  60

Qy   21  AspAspValSerGlyGlySerGlyValProGluSerAspArgProAlaGlyAlaGlnHis  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GATGAGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCCTGCCCAGCGCCAC  120

Qy   41  HisGlnLeuAsnGlyLysArgGlyProGlnSerAlaLysSerGluTrpThr  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CACCAGCTTAACGGGAAGCGGGGACCCTCAGAGTGCCAAGGAGTCAAGGAGTGGACC  180

Qy   61  ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyTyrAlaProGlySerGlyThr  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CCCTGCGGACCGCACCAAGGGCCAGGATGAAGGGCGCGGGGGCTACGCGCCCGGCAGCGGCACC  240

Qy   81  ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThr  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGACAGCTTCTGTTGCCACC  300

Qy  101  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GGGCCAGAACTCCCCCGTCCCCCGTGCCTTTGCCCCCAGGAAACCAGCCCTACCTGGGGGC  360

Qy  121  AspGlyThrProPheGlyCysProSerProSerAspProValGlu  140
         |||||||||||||||||||||||||||||||||||||||||||||
Db  361  GACGGGACCCCCTTTGGCTGTCCTCCCGGCAAAGAGAAGCCATCTGATCCCGTCGAG  420

Qy  141  TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr  160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TGGACCGTGATGGATGTCGTTGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA  480

Qy  161  AlaPheGlnGluGlnGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTCATCCAGCGCACAGATGTG  540

Qy  181  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys  200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  CTCACCGGCCTGTCCATCCGCCTCGGGCCGGCCCTGAAAATCTACGAGCACCACATCAAG  600

Qy  201  ValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly  217
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  GTGCTTCAGCAAGGCCACTTTGAGGATGACCCCGATGGCTTCTTAGGC  651
```

; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(651)
US-10-023-523-16

Alignment Scores:
Pred. No.:
Score: 2.38e-99   Length: 1208
                          1170.00   Matches: 217
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
                          13   Gaps: 0
DB:

US-09-976-740-7 (1-217) x US-10-023-523-16 (1-1208)

```
Qy    1  GluGlyArgValLeuGlyIleLysGluGluGluLeuAspAspAspGluAspGluGlu  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GAAGGACGAGTACTTGAGAAAAGAAGAAGAGAGAATGATGATGAAGATGAAGATGAAGAA  60

Qy   21  AspAspValSerGlyGlySerGlyValProGluSerAspArgProAlaGlyAlaGlnHis  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GATGAGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCCTGCCCAGCGCCAC  120

Qy   41  HisGlnLeuAsnGlyLysArgGlyProGlnSerAlaLysSerGluTrpThr  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CACCAGCTTAACGGGAAGCGGGGACCCTCAGAGTGCCAAGGAGTCAAGGAGTGGACC  180

Qy   61  ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyTyrAlaProGlySerGlyThr  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CCCTGCGGACCGCACCAAGGGCCAGGATGAAGGGCGCGGGGGCTACGCGCCCGGCAGCGGCACC  240

Qy   81  ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThr  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGACAGCTTCTGTTGCCACC  300

Qy  101  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GGGCCAGAACTCCCCCGTCCCCCGTGCCTTTGCCCCCAGGAAACCAGCCCTACCTGGGGGC  360

Qy  121  AspGlyThrProPheGlyCysProSerProSerAspProValGlu  140
         |||||||||||||||||||||||||||||||||||||||||||||
Db  361  GACGGGACCCCCTTTGGCTGTCCTCCCGGCAAAGAGAAGCCATCTGATCCCGTCGAG  420

Qy  141  TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr  160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TGGACCGTGATGGATGTCGTTGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA  480

Qy  161  AlaPheGlnGluGlnGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTCATCCAGCGCACAGATGTG  540

Qy  181  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys  200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  CTCACCGGCCTGTCCATCCGCCTCGGGCCGGCCCTGAAAATCTACGAGCACCACATCAAG  600

Qy  201  ValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly  217
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  GTGCTTCAGCAAGGCCACTTTGAGGATGACCCCGATGGCTTCTTAGGC  651
```

```
Db    601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

```
RESULT 6
US-10-616-187-16
;  Sequence 16, Application US20040013668A1
;  Publication No. US20040013668A1
;  GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/616,187
;  CURRENT FILING DATE: 2003-07-09
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SEQ ID NO 16
;  LENGTH: 1208
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(651)
US-10-616-187-16

Query Match:         15.00%
Alignment Scores:
Pred. No.:
Score:               1170.00
Percent Similarity:  100.00%
Best Local Similarity: 100.00%

US-09-976-740-7 (1-217) x US-10-616-187-16 (1-1208)

                     2.38e-99
                     Length:   1208
                     Matches:  217
                     Conservative: 0
                     Mismatches:   0
                     Indels:   0
                     Gaps:     0
```

```
Qy    1 GluGluArgValLeuGluLysGluGluGluAspAspGluAspGluAspGluGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGAAGATGAAGAA 60

Qy   21 AspAspValSerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGATGTCAGAGGCCTCTGAGAGTGCCCGAGAGTGCCCAGCAC 120

Qy   41 HisGlnLeuAsnGlyIleValArgGlyProGlnSerAlaLysGluValLysGluTrpThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAGCTTAACGGCGACGCGGGACCTCAGAGTGCCAAGGAGGTCAAGGAGTGGACC 180

Qy   61 ProCysGlyProHisGlnGlyArgGlyProAlaProGlySerGlyThr 80
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCTGCGGACCGCACCAGGGACGCGGGGCCGGCAGGAGGGCGGCACC 240

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGCGGAACAGCTTCTGTTGCCACC 300

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGAAAACCAGCCCTACCTGGGGCC 360

Qy  121 AspGlyThrProPheGlyCysProProGlyArgGlyLysGluLysProSerAspProValGlu 140
```

```
RESULT 7
US-09-945-527-6
;  Sequence 6, Application US/09945527
;  Publication No. US20030055888A1
;  GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. US20030055888A1e1 Nucleic Acid Molecules Encoding
;  TITLE OF INVENTION: Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 35800/237985
;  CURRENT APPLICATION NUMBER: US/09/945,527
;  CURRENT FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 65
;  SEQ ID NO 6
;  LENGTH: 1445
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  SOFTWARE: FastSEQ for Windows Version 4.0
US-09-945-527-6

Query Match:         10.00%
Alignment Scores:
Pred. No.:
Score:               1170.00
Percent Similarity:  100.00%
Best Local Similarity: 100.00%

US-09-976-740-7 (1-217) x US-09-945-527-6 (1-1445)

                     2.80e-99
                     Length:   1445
                     Matches:  217
                     Conservative: 0
                     Mismatches:   0
                     Indels:   0
                     Gaps:     0
```

```
Qy    1 GluGluArgValLeuGluLysGluGluGluAspAspGluAspGluAspGluGlu 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGAAGATGAAGAA 245

Qy   21 AspAspValSerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 GATGATGTCAGAGGCCTCTGAGAGTGCCCGAGAGTGCCCAGCAC 305

Qy   41 HisGlnLeuAsnGlyIleValArgGlyProGlnSerAlaLysGluValLysGluTrpThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 CACCAGCTTAACGGCGACGCGGGACCTCAGAGTGCCAAGGAGGTCAAGGAGTGGACC 365

Qy   61 ProCysGlyProHisGlnGlyArgGlyProAlaProGlySerGlyThr 80
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  366 CCCTGCGGACCGCACCAGGGACGCGGGGCCGGCAGGAGGGCGGCACC 425

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGCGGAACAGCTTCTGTTGCCACC 485

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGAAAACCAGCCCTACCTGGGGCC 545

Qy  121 AspGlyThrProPheGlyCysProProGlyArgGlyLysGluLysProSerAspProValGlu 140
```

```
Db  361 GACGGGACCCCCTTTGGCGTGTCCTCCCCGGCGCGCAAAGAGAGGAAGCCATCTGATCCGTCGAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  141 TrpThrValMetAspValValGluTyrProPheThrGluIleLeuAlaGlyProGluGlnAlaThr 160

Db  421 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGAGGCCAGGCGACA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  161 AlaPheGlnGluGlnGlnIleLeuAspGlyAlaLysSerLeuLeuLeuMetGlnArgThrAspVal 180

Db  481 GCTTTCCAAGACAGGAAAATTGATGGCAAAATCTTTGCTGCTCATGCAGCGCACAGATGTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 LeuThrGlyLeuSerIleAlaArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200

Db  541 CTCACCGGCCTGTTCATCGCCCTCGGGCAGCCCTGAAAATCTACAGACGACCATCAAG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspAspProAspGlyPheLeuGly 217

Db  601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 651
```

RESULT 8

US-09-976-740-45

; Sequence 45, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 45

; LENGTH: 1614

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1614)

US-09-976-740-45

Alignment Scores:

Score:	3.25e-99	
Pred. No.:	1170.00	Length:	1614
Percent Similarity:	100.00%	Matches:	217
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
		Indels:	0
DB:	9	Gaps:	0

US-09-976-740-7 (1-217) x US-09-976-740-45 (1-1614)

```
Qy      1 GluGluArgValLeuGlyLysGluGlyGluGluAspAspAspGluGlyGlu 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GAAGAGCGAGTACTTGAGAAGGAAGAGGAAGAAGATGATGAAGATGAAGAA 1023

Qy     21 AspAspValSerGlyValProGluSerAspArgProAlaGlyAlaGlnHis 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 GATGATGTGTCAGAGGGCTTCGAACCGTCCGAGAGTGACCGTGCCCAGCAC 1083

Qy     41 HisGlnLeuAsnGlyTyrArgGlyProGlnSerAlaLysGluArgValLys 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 CACCAGCTTAACGGCGAGCGGGGGGAGCGGGGGGACCTTCAGAGTGCCAAG 1143
```

Qy 546 GACGGGGACCCCTTTGGCCGTGCTCCCGGCGCAAAGAGAAGAAGCCATCTGATCCGTCGAG 605

Qy 141 TrpThrValMetAspValValGlyThrTyrPheThrGluIleAlaGlyPheProGlnAlaThr 160

Db 606 TGGACGGTGATGGATGTCGTGGAAATATTTACTGAGATCGCTGGATTCCCCGAGCAGGCGACA 665

Db 161 AlaPheGlnGluGlnGlnIleIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180

Qy 666 GCTTTCCAAGAGCAGGAAAATTGATGGCAAAATCTTTGCTGCTCATGCACGCACGAGATGTG 725

Db 181 LeuThrGlyLeuSerIleArgLeuGlyTyrGluIleTyrGluHisHisIleLys 200

Qy 726 CTCACCGGCCGCTGTCCATCCGCCAGCCCTGAAAATCTACGAGCACCACATCAAG 785

Db 201 ValLeuGlnGlnGlyHisPheGluAspAspAspAspGlyPheLeuGly 217

Qy 786 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCTTCTTAGGC 836

RESULT 9

US-10-671-242-45

; Sequence 45, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US/09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 45

; LENGTH: 1614

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1614)

US-10-671-242-45

Alignment Scores:

Pred. No.:	3.25e-99	Length:	1614
Score:	1170.00	Matches:	217

Db 1084 CACCAGCTTAACGGCGAGCGGGGGGAGCGGGGGGACCTTCAGAGTGCCAAGGAGGAGGGTTCAAGGAGGAGTGGACC 1143

Qy 61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyGlyArgGlyProAlaProGlySerGlyThr 80

Db 1144 CCCTGCGGACCACACCAGGGGCAGGATGAAGGGCGGTGGAGGGGGCCAGCCCCCGGGAGCGGGGCAC 1203

Qy 81 ArgGlnValPheSerMetAlaAlaLaMetAlaSnLysGlnLysGlyLysGlyGlyLysGlyThrAlaSerValAlaThr 100

Db 1204 CGCCAGGTGTTCTCCATGGCAGCGCCATGAACAAGCAGAAGGGGGAGAACAGGTTCTCGTTTGCCACC 1263

Qy 101 GlyValProAspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAla 120

Db 1264 GGCGTACCAGACTCCCCGTCCCCGGCCTTTGCCCCAGCGAAAACCAGCGCCTACCTGGGCGCC 1323

Qy 121 AspGlyThrProProheGlyCysProProGlyArgGlyLysGlyLysProSerAspProValGlu 140

Db 1324 GACGGGGACCCCCTTTGGCTGTCCGCCCCGGGGCGCAAAGAGAAGAAGCCATCTGATCCGTGGAG 1383

Qy 141 TrpThrValMetAspValValGlyThrTyrPheThrGluIleAlaGlyPheProGlnAlaThr 160

Db 1384 TGGACGGTGATGGATGTCGTGGAAATATTTACTGAGATCGCTGGATTCCCCGAGCAGGCGACA 1443

Qy 161 AlaPheGlnGluGlnGlnIleIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180

Db 1444 GCTTTCCAAGAGCAGGAAAATTGATGGCAAAATCTTTGCTGCTCATGCACGCACGAGATGTG 1503

Qy 181 LeuThrGlyLeuSerIleArgLeuGlyTyrGluIleTyrGluHisHisIleLys 200

Db 1504 CTCACCGGCCGCTGTCCATCCGCCAGCCCTGAAAATCTACGAGCACCACATCAAG 1563

Qy 201 ValLeuGlnGlnGlyHisPheGluAspAspAspAspGlyPheLeuGly 217

Db 1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCTTCTTAGGC 1614

```
Percent Similarity:        100.00%        Conservative:    0
Best Local Similarity:     100.00%        Mismatches:      0
Query Match:               100.00%        Indels:          0
DB:                        12             Gaps:            0

US-09-976-740-7 (1-217) x US-10-671-242-45 (1-1614)

Qy     1 GluGluArgValLeuGluLysGluGlyGluGluLeuAspAspAspGluAspGluGlu 20
Db   964 GAAGAGGAGACTACTTGAGAAGAAGAAGAGGAAGAAGATGATGATGAAGATGAAGAA 1023

Qy    21 AspAspValSerGluGlyLysSerGluValProGlySerAspArgProAlaGlyAlaGlnHis 40
Db  1024 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGGAGAGTGACCGTCCTTGACAGGTGCCCAGCAC 1083

Qy    41 HisGlnIleuAsnGlyGlyValGlyArgGlyHisProGlnSerAlaLysGluArgValLysGluTrpThr 60
Db  1084 CACCAGCTTAACGGCGGAGCGGGGACCTTCAGAGTGCCCAAGGAGAGGGTCAAGGAGTGGACC 1143

Qy    61 ProCysGlyProHisGlnIleuGlnAspGluValArgGlyProAlaProGlySerGlyThr 80
Db  1144 CCCTGCGGACCGCACCAGGAGATGAAGGGCGGGGGGCCAGCCCCGGGGCAGCGGCACC 1203

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
Db  1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGCGGAACAGCTTCTGTTGCCACC 1263

Qy   101 GlyProAspSerProValProLeuProProGlyTyrLysProAlaLeuProGlyAla 120
Db  1264 GGGCCAGACTCCCCCGTCCCCCTGCCTCCTGGCTACAAACCAGCCCTTACCTGGGGCC 1323

Qy   121 AspGlyTyrThrProPheGlyCysProGlyProGlyArgLysGlyLysProSerAspProValGlu 140
Db  1324 GACGGGACCCCCTTTGGCTGTCCCGGCCCCGGGCGAAAGGGCCATCTGATCCCGTCGAG 1383

Qy   141 TrpThrValMetAspValValGluTyrPheThrGlnAlaGlyPheProGluGlnAlaThr 160
Db  1384 TGGACCGTGATGGATGTCGTGGAATATTTTACTCAGGCTGGATTCCCGGAGCAGGCGACA 1443

Qy   161 AlaPheGlnGluGlnIleuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db  1444 GCTTTCCAAGAGCAGGAAAATTGATGGCAAAATCTTTGCTGCTCATGCAGCAGATGTG 1503

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLys 200
Db  1504 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAAATCTACGAGCACCACATCAAG 1563

Qy   201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db  1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 1614
```

RESULT 10
US-10-023-529-45
; Sequence 45, Application US/10023529
; Publication No. US20020129388A1
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10,023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-10-023-529-45

Alignment Scores:
```
Pred. No.:
Score:                3.2e-99        Length:          1614
Percent Similarity:   1170.00        Matches:         217
Percent Similarity:   100.00%        Conservative:    0
Best Local Similarity: 100.00%       Mismatches:      0
Query Match:          100.00%        Indels:          0
DB:                   13             Gaps:            0

US-09-976-740-7 (1-217) x US-10-023-529-45 (1-1614)

Qy     1 GluGluArgValLeuGluLysGluGlyGluGluLeuAspAspAspGluAspGluGlu 20
Db   964 GAAGAGGAGACTACTTGAGAAGAAGAAGAGGAAGAAGATGATGATGAAGATGAAGAA 1023

Qy    21 AspAspValSerGluGlyLysSerGluValProGlySerAspArgProAlaGlyAlaGlnHis 40
Db  1024 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGGAGAGTGACCGTCCTTGACAGGTGCCCAGCAC 1083

Qy    41 HisGlnIleuAsnGlyGlyValGlyArgGlyHisProGlnSerAlaLysGluArgValLysGluTrpThr 60
Db  1084 CACCAGCTTAACGGCGGAGCGGGGACCTTCAGAGTGCCCAAGGAGAGGGTCAAGGAGTGGACC 1143

Qy    61 ProCysGlyProHisGlnIleuGlnAspGluValArgGlyProAlaProGlySerGlyThr 80
Db  1144 CCCTGCGGACCGCACCAGGAGATGAAGGGCGGGGGGCCAGCCCCGGGGCAGCGGCACC 1203

Qy    81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
Db  1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGCGGAACAGCTTCTGTTGCCACC 1263

Qy   101 GlyProAspSerProValProLeuProProGlyTyrLysProAlaLeuProGlyAla 120
Db  1264 GGGCCAGACTCCCCCGTCCCCCTGCCTCCTGGCTACAAACCAGCCCTTACCTGGGGCC 1323

Qy   121 AspGlyTyrThrProPheGlyCysProGlyProGlyArgLysGlyLysProSerAspProValGlu 140
Db  1324 GACGGGACCCCCTTTGGCTGTCCCGGCCCCGGGCGAAAGGGCCATCTGATCCCGTCGAG 1383

Qy   141 TrpThrValMetAspValValGluTyrPheThrGlnAlaGlyPheProGluGlnAlaThr 160
Db  1384 TGGACCGTGATGGATGTCGTGGAATATTTTACTCAGGCTGGATTCCCGGAGCAGGCGACA 1443

Qy   161 AlaPheGlnGluGlnIleuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db  1444 GCTTTCCAAGAGCAGGAAAATTGATGGCAAAATCTTTGCTGCTCATGCAGCAGATGTG 1503

Qy   181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLys 200
Db  1504 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAAATCTACGAGCACCACATCAAG 1563

Qy   201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db  1564 GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 1614
```

RESULT 11
US-10-023-523-45
; Sequence 45, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)

US-10-023-523-45

Alignment Scores:
Pred. No.:
Score: 1170.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 13

Length:	1614
Matches:	217
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-976-740-7 (1-217) x US-10-023-523-45 (1-1614)

```
Qy      1 GluGluArgValLeuGlyLeuLysGluGluGlyLeuGluAspAspGluAspGluGlu    20
Db    964 GAAGAGCGAGTACTTGAGAAAGAAGAAGGAAGAATGAAGAAGATGAAGAAGA       1023

Qy     21 AspAspValSerGluGlyGlySerGluValProGlyGluSerAspArgProAlaGlyAlaGlnHis   40
Db   1024 GATGATGTGTCAGAGGGCTTCTGAAGTGCCCGAGAGTGACCGTCCTTGCAGGTGCCCAGCAC       1083

Qy     41 HisGlnLeuAsnGlyGlnArgGlyProGlnSerAlaLysGluValValLysGluTrpThr   60
Db   1084 CACCAGCTTAACGGGCAGCGGGGACCTCAGAGTGCCAAGGAGGTCAAAGAGTGGACC       1143

Qy     61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr   80
Db   1144 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGCGGGGCCAGCCCCTGGCAGGGCACC   1203
```

RESULT 12
US-10-616-187-45
Sequence 45, Application US/10/616,187
Publication No. US20040013668A1
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)

US-10-616-187-45

Alignment Scores:
Pred. No.:
Score: 1170.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 15

Length:	1614
Matches:	217
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-976-740-7 (1-217) x US-10-616-187-45 (1-1614)

```
Qy      1 GluGluArgValLeuGlyLeuLysGluGluGlyLeuGluGluAspAspGluAspGluGlu   20
Db    964 GAAGAGCGAGTACTTGAGAAAGAAGAAGGAAGAATGAAGAAGATGAAGAAGA        1023

Qy     21 AspAspValSerGluGlyGlySerGluValProGlyGluSerAspArgProAlaGlyAlaGlnHis   40
Db   1024 GATGATGTGTCAGAGGGCTTCTGAAGTGCCCGAGAGTGACCGTCCTTGCAGGTGCCCAGCAC       1083

Qy     41 HisGlnLeuAsnGlyGlnArgGlyProGlnSerAlaLysGluValValLysGluTrpThr   60
Db   1084 CACCAGCTTAACGGGCAGCGGGGACCTCAGAGTGCCAAGGAGGTCAAAGAGTGGACC       1143

Qy     61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr   80
Db   1144 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGCGGGGCCAGCCCCTGGCAGGGCACC   1203
```

```
Qy     81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThr   100
Db   1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGACACAGCTTCGTTGCCACC   1263

Qy    101 GlyProAspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAla   120
Db   1264 GGGCCAGACAGTCCCTCCCCGGTCCCCCCGGCCTTTGCCCCCCCAGGGAAACCAGCCCTACCTGGGGGC   1323

Qy    121 AspGlyThrProPheGlyTyrArgArgLysProSerAspProValGlu   140
Db   1324 GACGGGACCCCCTTTGGCTATCGGCGCCGGGAGAAGCCATCTGATCCGTCGAG       1383

Qy    141 TrpThrValMetAspValValGluTyrThrPheProGluGlnGlnAlaThr   160
Db   1384 TGGACCGTGATGGATGTCGTCGAAIATATTTACTGAGGGCTGGAGGCAGGGACA   1443

Qy    161 AlaPheGlnGluGlnGlnIleIleAspGlyGlyLysSerLeuLeuGlnArgThrAspVal   180
Db   1444 GCTTTCCAAGAGGCAGGAGAATTGATAGCGAAATCTTTGCTGCTCATGCAGCGCACAGAGTG   1503

Qy    181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysSerIleTyrGluHisHisIleLys   200
Db   1504 CTCACCGGCCTGTCCATCCGGCTCGGGCCAGCGCCCCTGAAAAGTCACGAGCACCACATCAAG   1563

Qy    201 ValLeuGlnGlnHisGlyHisSerPheGluAspAspAspGluAspGlyPheLeuGly   217
Db   1564 GTGCTTCAGCAGGCCACTTTGAGGATGATGACCCGGATGGCTTCTTAGGC         1614
```

RESULT 13
US-10-102-806-247
Sequence 247, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 247
LENGTH: 1336.
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (26)..
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1336)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-247

Alignment Scores:
Pred. No.:
Score: 1161.00
Percent Similarity: 99.08%
Best Local Similarity: 99.08%
Query Match: 99.23%
DB:

Length: 1336
Matches: 215
Conservative: 0
Mismatches: 2
Indels: 0
Gaps: 0

US-09-976-740-7 (1-217) x US-10-102-806-247 (1-1336)

```
Qy    1 GluGluArgValLeuGlyLysGluGlyLysAspAspGluAspGluAspGluGlu 20
Db   73 GAAGAGCGAGTACTTGAGAAAGGAAGAAGATGATGAAGATGAAGATGAAGAAGA 132

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGluGlyGlyThrAlaSerValAlaThr 100
Db 1204 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 1263

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db 1264 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTTACCTGGGGC 1323

Qy  121 AspGlyThrProPheGlyCysProProGlyTyrArgGlyValLysProSerAspProValGlu 140
Db 1324 GACGGGACACCCCTTTGGCTGTCCGCCCGGGTACCGAGGAGTCAAACCCAGCGACCCCGAG 1383

Qy  141 TrpThrValMetAspValValGlyTyrPheThrGluAlaGlyProGluGlnIleAlaThr 160
Db 1384 TGGACCGTGATGGAGTCGTCGGAATATTTACTGAGGGCTGGAATTCCCGGAGCAGGCGACA 1443

Qy  161 AlaPheGlnIleGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db 1444 GCTTTCCAAGCAGCAGAAAATTGATGGCAAAATCTTTGCTGTTCATCCGCACAGATGTG 1503

Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLeuLysIleTyrGluHisHisIleLeuLys 200
Db 1504 CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCACATCAAG 1563

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGlyGly 217
Db 1564 GTGCTTCAGCAGCAAGGCCCACTTTGAGGATGACCCCGATGGCTTCTTAGGC 1614
```

RESULT 14
US-09-962-055-12
Sequence 12, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
             Lees, Robert S.
             Arjoma, Anibal A.
             Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
             BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
             TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930

```
Qy   21 AspAspValSerGluGlyValProGluSerAspArgProAlaGlyAlaGlnHis 40
Db  133 GATGATGTGTCAGAGGGTGTCCCAGAAAGTGACCGGCCCGCAGGTGCCCAGCAC 192

Qy   41 HisGlnLeuAsnGlyLysArgGlyProGlnSerAlaLysGluGlyTrpThr 60
Db  193 CACCAGCTTAACGGCAAGCGAGGCCCCCAGAGTGCCAAGGAAGGGTGGACC 252

Qy   61 ProCysGlyProHisGlnGlyIleAspGlyGluGlyLysAspAspGluAspGluGlu 80
Db  253 CCCTGCGGACCGCACCAGGGCCCAGGATGAAGGGCGGGGGGGGCCAGCCGCAC 312

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGluGlyGlyThrAlaSerValAlaThr 100
Db  313 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 372

Qy  101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db  373 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTTACCTGGGGCC 432

Qy  121 AspGlyThrProPheGlyCysProProGlyTyrArgGlyValLysProSerAspProValGlu 140
Db  433 GACGGGACACCCCTTTGGCTGTCCGCCCGGGTACCGAGGAGTCAAACCCAGCGACCCCGAG 492

Qy  141 TrpThrValMetAspValValGlyTyrPheThrGluAlaGlyProGluGlnIleAlaThr 160
Db  493 TGGACCGTGATGGAGTCGTCGGAATATTTACTGAGGGCTGGATTCCCGGAGCAGGCGACA 552

Qy  161 AlaPheGlnIleGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db  553 GCTTTCCAAGCAGCAGAAAATTGATGGCAAAATCTTTGCTGTTCATCCGCACAGATGTG 612

Qy  181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLeuLysIleTyrGluHisHisIleLeuLys 200
Db  613 CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCACATCAAG 672

Qy  201 ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGlyGly 217
Db  673 GTGCTTCAGCAGCAAGGCCCACTTTGAGGATGACCCCGATGGCTTCTTAGGC 723
```

Left column

```
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;     NAME: Myers, Louis
;     REGISTRATION NUMBER: 35,965
;     REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617/542-5070
;     TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 1362 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     FEATURE:
;         NAME/KEY: Coding Sequence
;         LOCATION: 1...696
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
```

```
US-09-962-055-12

Alignment Scores:
Pred. No.:              5.93e-88
Score:                  1047.50
Percent Similarity:     95.45%
Best Local Similarity:  88.64%
Query Match:            89.53%
DB:
                        Length:        1362
                        Matches:       195
                        Conservative:  15
                        Mismatches:    7
                        Indels:        3
                        Gaps:          2
```

```
US-09-976-740-7 (1-217) x US-09-962-055-12 (1-1362)

Qy    1 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluGlu   20
        ||||||||||||||||||||||||||||||||||||||||||||::|:::::::
Db   37 GAGGAGCGAGTGCTTGAAAAAGGAGGAGGAGGAAGACGACGAGGACGAC        96

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla   38
        ||||||                |||||||||||||||||||||||||||||||||||||
Db   97 GACGACGACAGCTCGTCGTCCGAGGGTGCCCGAGACGCGATCGTCCCGCGGGGTGCG    156

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys   57
        ||||||||||||||||||   |||:::||||||||||||||||||||||
Db  157 CAGCATCACCAGCTGAATGGCGGCGGAGCCCAGACCCGCCAAGGAGCGCGGCCAAG    216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGly   77
        ||||||||||||||||||:::||||||||||||||||||||||||
Db  217 GAGTGGTCGCCTGTGTGGGCCCCCACCCTGGCCCAGGAGGAAGGGCGGCGGCCGCGGC   276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer   97
        ||||||||||||||||||||||||||:::||:::::::
Db  277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAATAGGAAGGGCGGCGGCCTCT   336

Qy   98 ValAlaThrGlyProAspSerProValProLeuProProGlyLysProAlaLeu   117
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 TCGACCACCGGGCCTGACTCCCCGGTCCCCCGGTGCCCCCGGGAAGCCCAGCCCTC   396

Qy  118 ProGlyAlaAspGlyThrProPheGlyCysProArgGlySGlyLysProSerAsp   137
        ||||||||||||||||:::::||||||||||||||||||||||||:::||
Db  397 CCAGGAGCGCCGATGGGAGACCCCCTTTGGCTGCCCCCGGGAAGCCCAGCC    456

Qy  138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyProGlu   157
        ||||||||||||||||||||||||||||||||||||||||||||||||:::||
Db  457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCCGGCCCTGAG   516

Qy  158 GlnAlaThrAlaPheGlnGlnGlnIleAspGlyLysSerLeuLeuMetGlnArg   177
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  517 CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGGAAGTCCCTGCTCATGCAGCGC   576

Qy  178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis   198
        |||||||||||||||||||||||||||||||||||||||||||||||||:::||
Db  577 ACCGAGTCCTCACCGGCCTGTCATCCCGCTGGGGCCAGCGTTGAAAATCATTGAGCAC   636

Qy  198 HisIleLysValLeuGlnGlnGlyHisPheLeuAspAspAspProAspGlyPheLeuGly   217
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  637 CATATCAAGGTGCTCCAGCAGGGGTCACTTCGAGGACGATGACCCGGACGGCTTCCTGGGA   696
```

Right column

```
RESULT 15
US-09-976-740-12
; Sequence 12, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
;     APPLICANT: Lees, Ann M.
;     APPLICANT: Lees, Robert S.
;     APPLICANT: Law, Simon W.
;     APPLICANT: Arjona, Anibal A.
;     TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;     TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;     TITLE OF INVENTION: ATHEROSCLEROSIS
;     FILE REFERENCE: 10797-004001
;     CURRENT APPLICATION NUMBER: US/09/976,740
;     CURRENT FILING DATE: 2001-10-12
;     PRIOR APPLICATION NUMBER: US 60/031,930
;     PRIOR FILING DATE: 1996-11-27
;     PRIOR APPLICATION NUMBER: US 60/048,547
;     PRIOR FILING DATE: 1997-06-03
;     PRIOR APPLICATION NUMBER: US 08/979,608
;     PRIOR FILING DATE: 1997-11-26
;     PRIOR APPLICATION NUMBER: 09/616,289
;     PRIOR FILING DATE: 2000-07-14
;     NUMBER OF SEQ ID NOS: 53
;     SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;     LENGTH: 1362
;     TYPE: DNA
;     ORGANISM: Oryctolagus cuniculus
;     FEATURE:
;         NAME/KEY: CDS
;         LOCATION: (1)...(696)
; US-09-976-740-12

Alignment Scores:
Pred. No.:              5.93e-88
Score:                  1047.50
Percent Similarity:     95.45%
Best Local Similarity:  88.64%
Query Match:            89.53%
DB:
                        Length:        1362
                        Matches:       195
                        Conservative:  15
                        Mismatches:    7
                        Indels:        3
                        Gaps:          2
```

```
US-09-976-740-7 (1-217) x US-09-976-740-12 (1-1362)

Qy    1 GluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAspGluGlu   20
        ||||||||||||||||||||||||||||||||||||||||||||::|:::::::
Db   37 GAGGAGCGAGTGCTTGAAAAAGGAGGAGGAGGAAGACGACGAGGACGAC        96

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla   38
        ||||||                |||||||||||||||||||||||||||||||||||||
Db   97 GACGACGACAGCTCGTCGTCCGAGGGTGCCCGAGACGCGATCGTCCCGCGGGGTGCG    156

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys   57
        ||||||||||||||||||   |||:::||||||||||||||||||||||
Db  157 CAGCATCACCAGCTGAATGGCGGCGGAGCCCAGACCCGCCAAGGAGCGCGGCCAAG    216

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGly   77
        ||||||||||||||||||:::||||||||||||||||||||||||
Db  217 GAGTGGTCGCCTGTGTGGGCCCCCACCCTGGCCCAGGAGGAAGGGCGGCGGCCGCGGC   276

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer   97
        ||||||||||||||||||||||||||:::||:::::::
Db  277 AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCATGAATAGGAAGGGCGGCGGCCTCT   336

Qy   21 AspAsp------ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla   38
        ||||||                |||||||||||||||||||||||||||||||||||||
Db   97 GACGACGACAGCTCGTCGTCCGAGGGTGCCCGAGACGCGATCGTCCCGCGGGGTGCG    156

Qy   39 GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys   57
        ||||||||||||||||||   |||:::||||||||||||||||||||||
Db  157 CAGCATCACCAGCTGAATGGCGGCGGAGCCCAGACCCGCCAAGGAGCGCGGCCAAG    216

Qy   98 ValAlaThrGlyProAspSerProValProLeuProProGlyLysProAlaLeu   117
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  337 TCGACCACCGGGCCTGACTCCCCGGTCCCCCGGTGCCCCCGGGAAGCCCAGCCCTC   396

Qy   58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGly   77
        ||||||||||||||||||:::||||||||||||||||||||||||
Db  217 GAGTGGTCGCCTGTGTGGGCCCCCACCCTGGCCCAGGAGGAAGGGCGGCGGCCGCGGC   276

Qy  157 CAGCATCACCAGCTGAATGGCGGCGGAGCCCAGACCCGCCAAGGAGCGCGGCCAAG    216

Qy  118 ProGlyAlaAspGlyThrProPheGlyCysProArgGlyLysProSerAsp   137
        ||||||||||||||||:::::||||||||||||||||||||||||:::||
Db  397 CCAGGAGCGCCGATGGGAGACCCCCTTTGGCTGCCCCCGGGAAGCCCAGCC    456
```

```
Qy  138  ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu  157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  457  CCCGTGGAGTGGACAGTCAATGGAGACGTCGTGGAGTACTTCACCGAGGGCGGCTTCCCTGAG  516

Qy  158  GlnAlaThrAlaPheGlnGluGlnIleLeuAspGlyLysSerLeuLeuMetGlnArg  177
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db  517  CAAGCCACCGCCTTTCCAGGAGCAGGAGATCGCAAGTCCCTGCTCATGCAGCGC  576

Qy  178  ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis  197
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db  577  ACCGATGTCCTCACCGGCCTGTCCATCCGGCCAGCGGTTGAAAATCTATGAGCAC  636

Qy  198  HisIleLysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly  217
              |||||||||||||||||||||||||||:::||||||||||||
Db  637  CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATCCCGGAAGGCTTCCTGGGA  696
```

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 19:55:37 ; Search time 3281.03 Seconds
(without alignments)
1975.018 Million cell updates/sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Title: US-09-976-740-7
Perfect score: 1170
Sequence: 1 EERVLEKEEEDDEDEDEE..........HIKVLQCGHFEDDPDGFLG 217

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODE3=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -QFMT=fastap -SUFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1.10232 @runat_10032004_094548_19551 -NCPU=6 -ICPU=3
-NO_NMAP -LARGEQUERY _NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estom:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	1170	100.0	1109	10	BE270805	BE270805 60943804
2	1095.5	93.6	858	10	BE564424	BE564424 60344543
3	1082	92.5	785	12	BI226646	BI226646 60951660
4	1072	91.6	996	13	BU174966	BU174966 AGENCOURT
5	1044	89.2	756	12	BM013469	BM013469 603638922
6	1030	88.0	921	13	BQ671165	BQ671165 AGENCOURT
7	1029	87.9	686	10	BE513784	BE513784 601315608
8	1026	87.7	590	10	BE621115	BE621115 601493936
9	1022	87.4	568	12	BM792162	BM792162 K-EST0072
10	1007	86.1	1056	12	BG298788	BG298788 602395526
11	992	84.8	774	12	BE891267	BE891267 61432095
12	988	84.4	600	12	BI987692	BI987692 3204-64 M
13	987	84.4	829	10	BE270987	BE270987 600943804
14	969	82.8	704	10	BF059975	BF059975 7k36508.x
15	967	82.6	600	12	BI985158	BI985158 3132-24 M
16	967	82.6	828	10	BE794500	BE794500 60190248
17	964	82.4	683	10	BE857956	BE857956 60159248
18	956	81.7	743	10	BF058118	BF058118 7k38e12.x
19	947.5	81.0	694	14	CA451506	CA451506 UI-M-FX0-
20	939	80.3	680	10	BE675122	BE675122 7f02h07.x
21	913	78.0	554	10	AW743445	AW743445 up67g05.y
22	911	77.9	533	10	BF190027	BF190027 236023 MA
23	911	77.9	707	10	BE746961	BE746961 60150888
24	894	76.4	906	12	BG116718	BG116718 602317440
25	884.5	75.6	1057	12	BM554748	BM554748 AGENCOURT
26	874	74.7	518	10	BE269536	BE269536 60184757
27	858	73.3	531	13	BX527955	BX527955 60184757
28	846	72.3	481	12	BG284882	BG284882 60249117
29	843	72.1	572	10	AA543367	AA543367 vj81c09.r
30	836	71.5	593	9	AI928488	AI928488 wp02e10.x
31	833.5	71.2	864	12	BG704736	BG704736 60268346
32	833	71.2	572	12	BM697252	BM697252 UI-E-DX0-
33	827	70.7	600	12	BI987677	BI987677 3204-48 M
34	822	70.3	580	10	BE257093	BE257093 60108824
35	821	70.2	583	9	AI660679	AI660679 wf23e11.x
36	818	69.9	590	9	AI123580	AI123580 Qa50b10.x
37	774.5	66.2	919	12	BI080921	BI080921 602878830
38	749.5	64.1	1022	13	BU538115	BU538115 AGENCOURT
39	743	63.5	812	14	BG762763	BG762763 602734678
40	714	61.0	432	14	W71214	W71214 me31c11.r1
41	686	58.6	518	10	BE481694	BE481694 167162 BA
42	681	58.2	411	10	AA160037	AA160037 ms666g04.r
43	679	58.0	862	13	BQ673964	BQ673964 602686346
44	678	57.9	512	10	AW515766	AW515766 hd88b04.x
45	677	57.9	487	9	AI186705	AI186705 qe82e05.x

ALIGNMENTS

RESULT 1
BE270805
LOCUS   BE270805   1109 bp   mRNA   linear   EST 13-JUL-2000
DEFINITION 6009438004F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966449 5',
            mRNA sequence.
ACCESSION   BE270805
VERSION   BE270805.1 GI:9144449
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1109)

RESULT 1 (continued)

```
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbe-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM69   row: h   column: 02
            High quality sequence stop: 749.
FEATURES             Location/Qualifiers
     source          1..1109
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2966449"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC 8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
```

US-09-976-740-7 (1-217) x BE270805 (1-1109)

```
Alignment Scores:
Pred. No.:                               Length:        1109
Score:                  1170.00          Matches:        217
Percent Similarity:     100.00%          Conservative:     0
Best Local Similarity:  100.00%          Mismatches:       0
Query Match:            10               Indels:           0
                                         Gaps:             0

9.29e-64
```

```
Qy    1  GluGluArgValLeuGlyLysGlyGluGluGluAspSerAspGluAspGluGlu   20
Db   39  GAAGAGCGAGTACTTGAGAAAGGAGAAGAGGAAGATGATAGTAAGATGAAGAGGAA   98

Qy   21  AspAspValSerGluGlyLysSerGluValProGluSerAspArgProAlaGlyAlaGlyAlaGlnHis   40
Db   99  GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCTGCAGGTGCCCAGCAC  158

Qy   41  HisGlnLeuAsnGlyLysArgGlyProGlnSerAlaLysLysGluTrpThr   60
Db  159  CACCAGCTTAACGGCGGAGGCGGCCACTCAGAGTGCCAAGGAGGGGTCAAGGAGCTGGAC  218

Qy   61  ProCysGlyProHisGlnGlyLnGlyArgGlyProAlaProGlySerGlyThr   80
Db  219  CCCTGGCGACCGCACCAGGGCCCAGGATGAAGGCCCCGGGGAGGTCAAGGCCAGCCGCAC  278

Qy   81  ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr  100
Db  279  CGCCAGGTGTTCTCCATGGCGGCCATGAACAACAAGGAAGGGGAACAGCTTCTGTTGCCACC  338

Qy  101  GlyProAspSerSerProSerProValProGluLeuProProGlyLysProAlaLeuProGlyAla  120
Db  339  GGGCCAGACTCCCCCGTCCCCGTGCCTTTACCCCCAGGCAAACCAGCCCTACCTGGGGGCC  398

Qy  121  AspGlyThrProPheGlyCysProSerAspProValGlu  140
Db  399  GACGGGACCCCTTTGGCTGTCCCGGCGAAGACCCCGATCCCGGTCGAG  458

Qy  141  TrpThrValMetAspValValGlyTyrPheThrGlnAlaThr  160
Db  459  TGGACCGTGATGGATGTCGTCGGATATTTTACTGAGGCTGGAATGACGAGGACA  518

Qy  161  AlaPheGlnGluGlnGlnIleAspAspGlyArgGlySerLeuLeuLeuMetGlnArgThrAspVal  180
Db  519  GCTTTCCAAGAGCAGCAGGAAATTGATGGCAGAAATCTTTGCGGCTCATGCAGCGACGATGTG  578

Qy  181  LeuThrGlyLeuSerIleArgLeuGlyTyrProAlaLeuLysIleTyrGluHisHisIleLys  200
Db  579  CTCACCGGCCTGTCCATCCGGCTCGGGCTACCCGGCCCTGAAAATCTTACGAGCACCACATCAAG  638

Qy  201  ValLeuGlnGlyLnGlyHisPheGluAspAspAspProAspGlyPheLeuGly  217
Db  639  GTGCTTCACCAAGGCCCACTTTGAGGATGATGACCCCGATGGGCTTCTTAGGC  689
```

RESULT 2

```
LOCUS       BE561424                 858 bp    mRNA    linear   EST 15-AUG-2000
DEFINITION  601344543F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677194 5',
            mRNA sequence.
ACCESSION   BE561424
VERSION     BE561424.1  GI:9805144
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE     Unpublished (1999)
  JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbe-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM352   row: f   column: 11
            High quality sequence stop: 709.
FEATURES             Location/Qualifiers
     source          1..858
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677194"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC 8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
```

US-09-976-740-7 (1-217) x BB561424 (1-858)

```
Alignment Scores:
Pred. No.:                               Length:         858
Score:                  1095.50          Matches:        211
Percent Similarity:      98.60%          Conservative:     0
Best Local Similarity:   93.63%          Mismatches:       3
Query Match:            10               Indels:           2
                                         Gaps:             0

3.2e-59
```

```
Qy    1  GluGluArgValLeuGlyLysGlyGluGluGluAspSerAspGluAspGluGlu   20
Db    1  GAAGAGCGAGTACTTGACAAAGGAGAAGAAGAGGAAGATGATAGTGATGAAGAGGAA   97

Qy   21  AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlyAlaGlnHis   40
Db   38  GAAGACGGAGTACTTGACAAAGGAGAAGAAGAGGAAGATGATAGTGATGAAGAGGAA   97
```

```
Db  98 GATGATGTGTCAGGAGGGGCCTCTGGAAGTGCCCCGGAGTGACCGTCCTGCAGGTGCACAC 157
Qy  41 HisGlnLeuAsnGlyGluArgGlyTyrProGlnSerAlaLysGlyValValLysGluTrpThr 60
Db 158 CACCAGCTTAACGCGGAGCGGGGGGGGACCTCAGAGTGCCAAGGAGGAGGGTCAAGGAGGACC 217
Qy  61 ProCysGlyProHisGlnGlyArgAspGluGlyArgGlyProAlaProGlySerGlyThr 80
Db 218 CCCTGCGACCGCACCA-GGCCAGGATGAAGGGGGGGGGGGGGCCAGGCGCGGCACC 276
Qy  81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 100
Db 277 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 336
Qy 101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db 337 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGGAAACCAGCCCTACCTGGGGCC 396
Qy 121 AspGlyThrProPheGlyCysProProGlyTyrArgLysSerProSerAspProValGlu 140
Db 397 GACGGGACCCCCTTTGGCTGTCCTCCCGGCTACAGAAAGAGCCCATCTGATCCCGTCGAG 456
Qy 141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyTyrPheProGluGlnAlaThr 160
Db 457 TGGACCGTGATGGAAGTCGTTGAGAATATTTTACTGAGGCTGGAATTCCCGGAGCAGGCGACA 516
Qy 161 AlaPheGlnLeuGluIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db 517 GCTTTCCAAGAGCAGAAAATTGATGGCAAAATCTTTGCTGCTCATGCAGCGGCACAGATGTG 576
Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLys 200
Db 577 CTCACCGGCGTGTC-ATCCGGCCTCGGGCACCCCTGAAAATCTACAGACAGCCACATCAAG 634
Qy 201 ValLeuGlnGlnGlyHisPheGluLeuAspSerAspSerProAspGly 214
Db 635 GTGCTTCAGCAAGGCCCACTTTGAGGATGATGACCCGATGGT 676
```

RESULT 3

LOCUS   BI226646   785 bp   mRNA   linear   EST 11-JUL-2001

DEFINITION   602951660F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5095742 5',
           mRNA sequence.

ACCESSION   BI226646

VERSION   BI226646.1   GI:14680090

KEYWORDS   EST.

SOURCE   Homo sapiens (human)

  ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 785)

  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

  JOURNAL   Unpublished (1999)

COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1866 row: h column: 15
           High quality sequence stop: 785.

FEATURES   Location/Qualifiers
     source   1..785
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5095742"
                    /tissue_type="Burkitt lymphoma"

ORIGIN

Alignment Scores:
Pred. No.:   2.02e-58   Length: 785
Score: 1082.00   Matches: 214
Percent Similarity: 98.62%   Conservative: 0
Best Local Similarity: 98.62%   Mismatches: 0
Query Match: 92.48%   Indels: 3
DB: 12   Gaps: 0

US-09-976-740-7 (1-217) x BI226646 (1-785)

```
Qy   1 GluGluValValLeuGlnValHisGluGluLeuAspAspAspAspGluAspGluGlu 20
Db   1 GAAGACGTAGTACTTGAGAAGAGAAGAAGAACAGATGAATGAAGATGAAGGAA 59
Qy  21 AspAspValSerGluGlyGluGlyValValSerGluArgProAlaGlyAlaGlnHis 40
Db  59 .GATGATGTGTCAGGAGGGGCCTCTGGAAGTGCCCCGGAGTGACCGTCCTGCAGCAC 118
Qy  41 HisGlnLeuAsnGlyGluArgGlyTyrProGlnSerAlaLysGlyValValLysGluTrpThr 60
Db 119 CACCAGCTTAACGCGGAGCGGGGGGGGACCTCAGAGTGCCAAGGAGGAGGGTCAAGGAGGACC 178
Qy  61 ProCysGlyProHisGlnGlyArgAspGluGlyArgGlyProAlaProGlySerGlyThr 80
Db 179 CCCTGCGACCGCACCA-GGCCAGGATGAAGGGGGGGGGGGGGCCAGGCGCGGCACC 238
Qy  81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 100
Db 239 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 298
Qy 101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
Db 299 GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGGAAACCAGCCCTACCTGGGGCC 358
Qy 121 AspGlyThrProPheGlyCysProProGlyTyrArgLysSerProSerAspProValGlu 140
Db 359 GACGGGACCCCCTTTGGCTGTCCTCCCGGCTACAGAAAGAGCCCATCTGATCCCGTCGAG 418
Qy 141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyTyrPheProGluGlnAlaThr 160
Db 419 TGGACCGTGATGGAAGTCGTTGAGAATATTTTACTGAGGCTGGAATTCCCGGAGCAGGCGACA 477
Qy 161 AlaPheGlnLeuGluIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
Db 478 GCTTTCCAAGAGCAGAAAATTGATGGCAAAATCTTTGCTGCTCATGCAGCGGCACAGATGTG 537
Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLys 200
Db 538 CTCACCGGCGTGTC-ATCCGGCCTCGGGCACCCCTGAAAATCTACAGACAGCCACATCAAG 597
Qy 201 ValLeuGlnGlnGlyHisPheGluLeuAspSerAspSerProAspGlyPheLeuGly 217
Db 598 GTGCTTCAGCAAGGCCCACTT-GAGGATGATGACCCGATGGGCTTCTTAGGC 657
```

RESULT 4

LOCUS   BU174966   996 bp   mRNA   linear   EST 04-SEP-2002

DEFINITION   AGENCOURT_8073899 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6087267
           5', mRNA sequence.

ACCESSION   BU174966

VERSION   BU174966.1   GI:22688950

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2323 row: j column: 04
 High quality sequence stop: 592.

FEATURES Location/Qualifiers
source 1..996
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6087267"
 /tissue_type="epidermoid carcinoma, cell line"
 /clone_lib="NIH_MGC_102"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC library."

ORIGIN

US-09-976-740-7 (1-217) x EU174966 (1-996)

Alignment Scores:

Pred. No.:	1		
Score:	1.4e-57	Length:	996
	1072.00	Matches:	206
Percent Similarity:	95.85%	Conservative:	2
Best Local Similarity:	94.93%	Mismatches:	6
Query Match:	91.62%	Indels:	3
	13	Gaps:	1

```
Qy   1  GluGluArgValLeuGlyLysGluGluGluLeuAspAspAspGluAspGlyGlu  20
        ||||||||||||||||||||||||||||||||||||||||||||
Db  145  GAAGAGCGAGTACTTGAGAAAGAGAAGAGGAAGAAGAGATGAT-----GATGAAGATGAAGAA  198

Qy  21  AspAspValSerGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis  40
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  199  GATGATGTGTCAGAGGGGTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGAGCTGCAGCAC  258

Qy  41  HisGlnLeuAsnGlyGlyArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr  60
        ||||||||||||||||||||||||||||||||||||||||||||
Db  259  CACCAGCTTAACGGCGGACGGGGACAGTCCAAGGAGAGGGTCAAGGAGTGGACC  318

Qy  61  ProCysGlyProHisGlnGlyGlnAspGlyArgGlyProAlaProGlySerGlyThr  80
        ||||||||||||||||||||||||||||||||||||||||||||
Db  319  CCCTGCGGACCACACAGGGGCCAGGATGGAAGGGCGGGCCCAGCCCGGCAGCGGCCACC  378

Qy  81  ArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyGlyThrArgLeuSerValAlaSerAlaThr  100
        |||||||||||||||||||||||||||||||||||||||||||
Db  379  CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGGAGGAGGAACAGCTTCGTTGCCACC  438

Qy  101  GlyProGlyAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
         |||||||||||||||||||||||||||||||||||||||||
Db  439  GGGCCAGGAGACTCCCCGTCCCCGGTGCCCTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC  498
```

RESULT 5
BM013469
LOCUS BM013469 756 bp mRNA linear EST 30-OCT-2001
DEFINITION 603892ZF1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5415292 5',
 mRNA sequence.
ACCESSION BM013469
VERSION BM013469.1 GI:16527823
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM2059 row: k column: 05
 High quality sequence stop: 752.

FEATURES Location/Qualifiers
source 1..756
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5415292"
 /tissue_type="mammary adenocarcinoma, cell line"
 /clone_lib="NIH_MGC_87"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

US-09-976-740-7 (1-217) x BM013469 (1-756)

Alignment Scores:

Pred. No.:	1		
Score:	4.65e-56	Length:	756
	1044.00	Matches:	197
Percent Similarity:	99.49%	Conservative:	0
Best Local Similarity:	99.49%	Mismatches:	1
Query Match:	89.23%	Indels:	1
	12	Gaps:	0

```
Qy  121  AspGlyThrProPheGlyCysProProGlyArgLysProSerProSerAspArgProValGlu  140
         ||||||||||||||||||||||||||||||||||||||||||
Db  499  GACGGGACCCCCTTTGGGCTGTCCTCCCGGGCGCCAAAGAGAAGGAAGCCATCTGATCCGTCGAG  558

Qy  141  TrpThrValMetAspValValGluTyrPheThrGlnAlaGlyProGluGluGlnIleAlaThr  160
         ||||||||||||||||:::||||||||||||||||||||||||
Db  559  TGGACCGTGATGGATGTCGTCCAAATATTTACTGAGGCTGGATTCCCGGAGCAAGCGACA  618

Qy  161  AlaPheGluGlyGlnGluIleAspGlyGlyLysSerLeuLeuLeuMetGlnArgThrAspVa  180
         ||||||||||||||||||||||||||||||||||||:::|||
Db  619  GCTTTTCCAGGAACAGGAAAATTGATGGCAAATCTTTTGCCGGCTCATGCAGCGCCACAAATGT  678

Qy  180  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLeuLysSerIleTyrGlnHisHisIleGlu  200
          ||||||||||||||||||||||||||||||||||||||||
Db  679  GCTCACCGGCCTGTCCATCCGGCTCGGGCCAGCCCTGAAAAATCTAGGAGCACCCCATCAA  738

Qy  200  SerValLeuGlnIleGlyHisSerPheGluAspAspAspProAspGlyPheLeu  216
          ||||||||||||||||||||||||||||||||||||||||
Db  739  GGTGCTTCAGCAAGGGCCCTTTGCGGATGATGACCCCGATGGCCTTCTT  787
```

```
Qy    20  GluAspAlaValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGln  39
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACACCGTCCCTGGAGGTGCCCAG  60

Qy    40  HisHisGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLysGluGlyTrp  59
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CACCACCAGCTTAACGGCGAGGGGGGACCTTCAGAGTGTCCAAGGAGGGGTGG  120

Qy    60  ThrProCysGlyProHisGlnGlyLysAspGluGlyArgGlyProAlaProGlySerGly  79
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ACCCCCTGCGGACCCCACCA-GGCCAGGATGAAGGGGGCGGGGGCCAGCCCCCGGGCAGGGGC  179

Qy    80  ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAla  99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180  ACCCGGCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCC  239

Qy   100  ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGly  119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240  ACCGGGCCAGACTCCCCGTCCCCGGTCCCTTTGCCCCCAGGAAACCAGCCCTACCTGGG  299

Qy   120  AlaAspGlyThrProPheGlyCysProGlyTyrArgLysSerProSerAspProVal  139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300  GCCGACGGGACCCCCTTTGGCTGTCCTCCGGGGTACCGCAAAGAGAACCCATCTGATCCCGTC  359

Qy   140  GluTrpThrValMetAspValValGlyTyrPheThrGluAlaGlyPheProGluGlnIleAla  159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360  GAGTGGACCGTGATGGAATGTGTCGGATATTTTACTGAGGCTGGATTCCCGGAGCAGGGCG  419

Qy   160  ThrAlaPheGlnGlnGlnGlnIleAspGlyLysSerSerLeuLeuLeuMetGlnArgThrAsp  179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420  ACAGCTTTCCAAGAGCAGGAAAATTGATGGGAAATCTTCTGCTCATGCAGCGGACAGAT  479

Qy   180  ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIle  199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480  GTGCTCACCGGCCTGTCCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCACATC  539

Qy   200  LysValLeuGlnGlnGlnHisPheGluAspSerAspProGlyProGlyPheLeuGly  217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540  AAGGTGCTTCAGCAGCAGCACTTTGAGGATGATGACCCCGGATGGCTTCTTAGGC  593
```

```
RESULT 6

LOCUS         BQ671165         921 bp    mRNA     linear     EST 15-JUL-2002
DEFINITION    AGENCOURT_8032664 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6213736
              5', mRNA sequence.
ACCESSION     BQ671165
VERSION       BQ671165.1   GI:21781999
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 921)
  AUTHORS     Mammalian Gene Collection (MGC)
  TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL     Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2379 row: o column: 17
              High quality sequence stop: 538.

FEATURES             Location/Qualifiers
     source          1..921
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6213736"
```

```
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC 102"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.:                4.44e-55
Score:                    1030.00
Percent Similarity:       92.66%    Matches:        199    Length:       921
Best Local Similarity:    91.28%    Conservative:     3    Mismatches:    12
Query Match:              88.03%    Mismatches:      12    Indels:         4
DB:                       13        Indels:           4    Gaps:           1
```

```
US-09-976-740-7 (1-217) x BQ671165 (1-921)
```

```
Qy     1  GluGluArgValLeuGluLysGluGluGluGluLeuAspAspAspGluAspGluAspGluGlu  20
          ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db   145  GAAGAGCGAGTACTTGAGAAAGAGGAAGAAGAGAAGAAGAAGATGAT------GATGAAGATGAAGAA  198

Qy    21  AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHisHis  40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199  GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCCGCAGGTGCCCAGCAC  258

Qy    41  HisGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLysGluGlyTrpThrThr  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   259  CACCAGCTTAACGGCGAGGGGGGACCTCAGAGTGCCAAGGAGGGGTGGACC  318

Qy    61  ProCysGlyProHisGlnGlyLysAspGluGlyArgGlyProAlaProGlySerGlyThr  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   319  CCCTGCGGACCCCACCAGGCCAGGATGAAGGGGGCGGGGGCCAGCCCCCGGGCACC  378

Qy    81  ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379  CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC  438

Qy   101  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439  GGGCCAGACTCCCCGTCCCCGGTCCCTTTGCCCCCAGGAAACCAGCCCTACCTGGGGCC  498

Qy   121  AspGlyThrProPheGlyCysProGlyTyrArgLysSerProSerAspProValGlu  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   499  GACGGGACCCCCTTTGGCTGTCCTCCGGGGTACCGCAAAGAGAACCCATCTGATCCCGTCGAG  558

Qy   141  TrpThrValMetAspValValGlyTyrPheThrGluAlaGlyPheProGluGlnIleAlaThr  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   559  TGGACCGTGATGGAATGTGTCGGATATTTTACTGAGGCTGGATTCCCGGAGCAGGGCGACA  618

Qy   161  AlaPheGlnGlnGlnIleAspGlyLysSerSerLeuLeuLeuMetGlnArgThrAspVal  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   619  GCTTTCCAAGAGCAGGAAAATTGATGGGAAATCTTCTGCTCATGCAGCGGACAGTGTG  678

Qy   181  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys  200
          |||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db   679  CTTCCCGGGCCGTGTTCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCAGGATCAAG  738

Qy   201  ValLeuGln-GlnGlyHisPheGlu-AspAspAspProGlyProGlyPheLeu  216
          ||| |||||||||| ||||:::|||||||||||||||||||||||||||
Db   739  GGGCTTTCCGCAGGGCGCCCTTGAGGGGTGAATGACACCCGAGGGGCTTCTTA  788
```

```
RESULT 7

LOCUS         BE513784         686 bp    mRNA     linear     EST 07-AUG-2000
DEFINITION    601311508F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634417 5',
              mRNA sequence.
ACCESSION     BE513784
```

```
VERSION     BE513784.1  GI:9720996
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 686)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM328 row: p column: 02
            High quality sequence stop: 642.
FEATURES             Location/Qualifiers
     source          1..686
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3634417"
                     /tissue_type="Burkitt lymphoma"
                     /clone_lib="NIH_MGC_8"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGACAGAG(G). Size-selected >500bp for average
                     insert size 1.8kb Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

US-09-976-740-7 (1-217) x BE513784 (1-686)

Alignment Scores:
Pred. No.:                  3.61e-55          Length:        686
Score:                      1029.00           Matches:       209
Percent Similarity:         96.76%            Conservative:  0
Best Local Similarity:      96.76%            Mismatches:    6
Query Match:                87.95%            Indels:        5
DB:                         10                Gaps:          0
```

```
Qy     2 GluArgValLeuGlu-LysGluGlyGlnGluValAspAspAspGluAspGluGluAs  21
         ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    42 GAGCGAGTACTTGAGCAAAGAAAGAGGAAGGATCATGATGAAGATGAAGATGAGGAAGA 101

Qy    21 pAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHisHi  41
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   102 TGATCGTCAGAGGGCTCGAAGGTGCCCGAGAGTGACGGTCC-GCAGGTGCCCAGCACCA 161

Qy    41 sGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLysGluValLysGluTrpThrPr  61
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   162 CCAGCTTAACGGCGGAGCGGGGACCTCAAGGAGTGCCCAAGGAGGAGGTGGACCC 221

Qy    61 oCysGlyProHisGlnValGlnAspGluGlyGlyArgGlyProAlaProGlySerGlyThrAr  81
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   222 CTGCGGACCCCACCAGGGCCAGGATGAAGGGCGGGGGCCCAGCCCCCGGCAGCGGGCACCCG 281

Qy    81 gGlnValPheSerValMetAlaAlaMetAsnLysGluGlyGlyTyrThrAlaSerValAlaThrGl 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   282 CCAGGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGGGAACAGCTTTGTTGCCACCGG 341

Qy   101 yProAspSerSerProValProLeuProGlyProGlyAlaAs 121
         ||||||||||||||||||||||||||||||||||||||||||
Db   342 GCCAGACTCCCCGGTCCCCCTGCCTTTGCCCCAGGCAAACCAGCCCCTACCTCGGGCCGA 401
```

```
RESULT 8
LOCUS       BE621115         590 bp     mRNA      linear    EST 20-OCT-2000
DEFINITION  601939369F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896097 5',
            mRNA sequence.
ACCESSION   BE621115
VERSION     BE621115.1  GI:9892053
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9688 row: g column: 10
            High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1..590
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3896097"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_70"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.1 kb. Library constructed by Life
                     Technologies."
ORIGIN

US-09-976-740-7 (1-217) x BE621115 (1-590)

Alignment Scores:
Pred. No.:                  4.66e-55          Length:        590
Score:                      1026.00           Matches:       189
Percent Similarity:         100.00%           Conservative:  0
Best Local Similarity:      100.00%           Mismatches:    0
Query Match:                87.69%            Indels:        0
DB:                         10                Gaps:          0
```

```
Qy   121 pGlyThrProPheGlyCysProProGlyProGlyArgLysGluGlySerAspProValGluThr 141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   402 CGGGGACACCCCCTTTGGCTGTCCTCCCGGGCCCAGGGAGGAAGAGCCCATCTGATCCGTCGGAGTG 461

Qy   141 pThrValMetAspValValGlyThrPheThrGlyAlaGlyPheProGluGlnAlaThrAl 161
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   462 GACCGTGATGGATGTCGTCGGAATATTTACTGAGGTGGATTCCCGAGCAGGCGACGAGC 521

Qy   161 aPheGlnGluGlnGlnLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValIle 181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   522 TTTCCAAGAGCAGCAAAACCGATGGCAAATCTTTGCTCCTCATGCAGCGAACTGATGTGCT 581

Qy   181 uThrGlyLeuSerIleArgLeuGlyProAlaLeuLeuLysIleTyrGluHisHisIleIleLysVa 201
         ||||||||||||||||||||||||||||||||||||||| |||||||| |||||||||||
Db   582 CACCGGCCTGTCCATCCGGCTCGGGCCCGCAGCCCTGAAATC-TACGAGCC-CACATCAAGGT 639

Qy   201 lLeuGlnGlnHisGlnPheGluAspAspArgProAlaProGlyPheLeu 216
         ||||||||||  |||||||||||||| |||||||||||||||| |
Db   640 GCTCAGCCAGC--CACTTTGAGGGTGGATTG-CCGGATGGGCTTCTTA 682

Qy    26 GlySerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGly 45
```

FEATURES   Location/Qualifiers
     source   1..568
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="S22SNU16n1-15-C02"
                   /sex="F"

High quality sequence stop: 568.
Plate: 15 row: C column: 02
Email: yongsung@mail.kribb.re.kr
Fax: +82-42-860-4409
Tel: +82-42-860-4470
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Korea Research Institute of Bioscience & Biotechnology
Genome Research Center

COMMENT   Contact: Kim YS
                  21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
TITLE   Kim,Y.S.
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                  Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
REFERENCE   1 (bases 1 to 568)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SOURCE   Homo sapiens
                  Homo sapiens (human)
KEYWORDS   EST.
VERSION   BM792162.1   GI:19140394
ACCESSION   BM792162
DEFINITION   K-EST0072322 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-15-C02
                  5', mRNA sequence.
LOCUS   BM792162   568 bp   mRNA   linear   EST 05-MAR-2002

RESULT 9
BM792162

Db   1   GGCTCTGAAGTGCCCAGAGGTGACCGTTCTCCAGGTGCCCAGCACCACCAGCTTAACGGC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   46 GluArgGlyGlyProGlnSerAlaLysGluArgValLysGlyThrProCysGlyProHis   65

Db   61 GAGCGCGGGGACCTCAGAGTGCCCAAGGAGAGGGTCAAGGAGTGGACCCCCTCGCGGACAC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   66 GlnGlyGlnAspGluArgValArgGlyAlaProGlySerGlyThrArgGlnValPheSer   85

Db   121 CAGGGCCAGGATGAAGGGCGGGGGGGGCCAGGCCCCGGGGAGCGCCACCCCGCAGCTGCTC   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   86 MetAlaAlaAsnLysGluGlyGlyGlyThrAlaSerValAlaAlaThrGlyProAspSerPro   105

Db   181 ATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACGGGACCGGACTCCCCG   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   106 SerProValProLeuProProGlyGlyLysProGlyAlaAspGlyAlaThrProPhe   125

Db   241 TCCCCCCGTGCCTTTGCCCCCAGGCAAACAGCCCTACCTCGGGCCGACCCCCTTT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   126 GlyLysProProGlyArgGlyLysProSerAspProValGluTrpThrValMetAsp   145

Db   301 GGCTGGTCCTCCCGGGGGCAAAGAGAAGCCATCTGATCCCGTCGAGTGACCGTGATGGAT   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   146 ValValGluThrGlyThrGlyIleGlyPheProGlyLeuAlaGlyProAlaThrAlaPheGlyGlnGlnGln   165

Db   361 GTCGGTCGAAATATTTTACTGAGGCTGATTCCCGGACGAGCAGGCCGACAGCTTCCAAGAGACAG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   166 GlyIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer   185

Db   421 GAAATTGATGGCAAAATCTTTGCTGCTCATGCGACGCCACCACGATGGTCCTCACCGGCTGTCC   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   186 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLysValValValVal   205

Db   481 ATCCGGCCTCGGGCCCAGCCCTCTGAAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGC   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   206 HisPheGluAspAspAspProAspGly   214

Db   541 CACTTTGAGGATGAATGACCCCGATGGT   567
          |||||||||||||||||||||||||||

ORIGIN

/tissue_type="Ascites"
/cell_type="lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

Alignment Scores:
Pred. No.:
Score: 7.93e-55
Length: 568
Matches: 188
Percent Similarity: 1022.00
Best Local Similarity: 100.00%
Query Match: 87.35%
DB: 12

US-09-976-740-7 (1-217) x BM792162 (1-568)

Qy   28 GluValProGluSerAspAlaGlyProAlaGlyValAlaGlnHisHisGlnLeuLeuAsnGlyGluArg   47
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3   GAAGTGCCCGAGAGTGACCGTTCTCCTGCAGGTGCCCAGCACCACCAGCTTAACGGCGAGCGG   62

Qy   48 GlyProGlnSerGluArgValArgGlyAlaProGlySerGlyThrArgGlnValPheSerMetAlaVal   67
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 GGACCTCAGAGTGCCCAAGGAGAGGGTCAAGGAGTGGACCCCCTCGCGGACACCAGGGC   122

Qy   68 GlnAspGluArgGlyTyrProAlaProGlySerGlyThrArgGlnValPheSerMetAla   87
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 CAGGATGAAGGGCGGGGGGGGCCAGGCCCCGGGGAGCGCCACCCCGCAGCTGCTCATGGCA   182

Qy   88 AlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaAlaThrGlyProAspSerProSerPro   107
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 GCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACGGGACCGGACTCCCCGTCCCCCC   242

Qy   108 ValProLeuProProGlyGlyLysProGlyAlaAspGlyAlaThrProPheGlyCys   127
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 GTGCCCTTTGCCCCCAGGCAAACAGCCCTACCTCGGGCCGACCCCCTTTGGCTGT   302

Qy   128 ProProGlyArgGlyLysProSerAspProValGluTrpThrValMetAspValVal   147
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 CCTCCCGGGGGCAAAGAGAAGCCATCTGATCCCGTCGAGTGGACCGTGATGGATGTCGTC   362

Qy   148 GluTyrPheThrGlyAlaGlyPheProGluGlnGlnAlaThrAlaAlaPheGlnGlnGlnGlnIle   167
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 GAATATTTTACTGAGGCTGGATTCCCGGACGAGCAGGCCGACAGCTTCCAAGAGCAGAAATT   422

Qy   168 AspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerIleArg   187
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 GATGGCAAAATCTTTGCTGCTCATGCGACGCCACCACGATGGTCCTCACCGGCTGTCCATCCGC   482

Qy   188 LeuGlyProAlaLeuLysIleTyrGluHisHisIleLeuLysValLeuGlnGlnGlyHisPhe   207
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 CTCCGGGCCCAGCCCTGAAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT   542

Qy   208 GluAspAspAspProAspGlyPhe   215
          |||||||||||||||||||||||||
Db   543 GAGGATGAATGACCCCGATGGCTTC   566

RESULT 10
BG298788

ACCESSION   BG298788
VERSION   BG298788.1   GI:13063792
DEFINITION   603396526F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511167 5',
                  mRNA sequence.
LOCUS   BG298788   1056 bp   mRNA   linear   EST 21-FEB-2001

KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
   ORGANISM   Mus musculus
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1056)
   AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
       National Institutes of Health, Mammalian Gene Collection (MGC)
   TITLE   Unpublished (1999)
   JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
       Email: cgapbs-r@mail.nih.gov
       Tissue Procurement: The Cepko Laboratory
       cDNA Library Preparation: Life Technologies, Inc.
       cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
       DNA Sequencing by: Incyte Genomics, Inc.
       Clone distribution: MGC clone distribution information can be
       found through the I.M.A.G.E. Consortium/LLNL at:
       http://image.llnl.gov
       Plate: LLAM10394 row: c column: 08
       High quality sequence stop: 752.
FEATURES   Location/Qualifiers
   source   1..1056
       /organism="Mus musculus"
       /mol_type="mRNA"
       /db_xref="taxon:10090"
       /clone="IMAGE:4511167"
       /tissue_type="retina"
       /lab_host="DH10B (phage-resistant)"
       /clone_lib="NIH_MGC_94"
       /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
       Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
       Average insert size 3.3 kb. Library enriched for
       full-length clones and constructed by Life Technologies.
       Note: this is a NIH_MGC Library."
ORIGIN

US-09-976-740-7 (1-217) x BG298788 (1-1056)

Alignment Scores:
Pred. No.:   1.44e-53
Score: 1007.00
Percent Similarity: 96.00%
Best Local Similarity: 92.00%
Query Match: 86.07%

Length: 1056
Matches: 184
Conservative: 8
Mismatches: 8
Indels: 0
Gaps: 0

Qy   18 AspGluGluAspAlaValSerGluGlyValProGluSerAspArgProAlaGly 37
         :::||||||||||||||||||||||||||||||||||||||||||||::||
Db   12 GAGGAGGAGGACAATGTATCTGAGGGCTCAGAAGCTGACGCCCCGCAGGT 71

Qy   38 AlaGlnHisHisGlnLeuAsnGlyGluArgGlyArgGlyArgValLys 57
         |||||||||||||||::|||||||||||||||||||||||||||||||
Db   72 GCTCAGCACCATCAGATTAATGGAGAGCGGGAGGGCCCTCAGAGTGGTCAAG 131

Qy   58 GluTrpThrProCysGlyProHisGlnGlyTyrGlnAspGluGlyArgGlyTyrProAlaProGly 77
         |||||||||::|||||||||||||||||||||||||||||||||||||||
Db   132 GAGTGGTGCGCCCTGTGGACCCTACCAGGGCGGATGAGGACGCCACCAGACCTGGC 191

Qy   78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
         |||||||||||||||||||||||||||||||||||||||||||:::|||
Db   192 AGCTGCACAGGGCAGGTGTTCCCGATGACAGCTGAATAAAAAGAAGGGGGATCAGCTTGT 251

Qy   98 ValAlaThrGlyTyrProSerProSerProValProLeuProProGlyLysProAlaLeu 117
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   252 GTTGGAGCAGCTCAGATTCTCCAATCTCCGGGTGCCTTTGCCTCCAGGAAAACCAGCTCTA 311

Qy   118 ProGlyAlaAspGlyThrProHisGlyCysProProGlyArgLysGlyLysProSerAsp 137
         |||||||||||||||||||||||||||||||||||||||||:::|||
Db   312 CCTGGGGCTGATGGAGACACCTTTGGCGTGTCTTCCCGGGCGAAGGAGAAGGGACAGAC 371

Qy   138 ProValGlyTrpThrValMetAspValValGlyTyrPheThrGluAlaGlyPhePrpGlu 157
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   372 CCAGTGGGAGTGGACAGTCATGGACGTGGAAATACTTCACTGAGGCGGGCTTCCCAGAG 431

RESULT 11
BE891267
   LOCUS   BE891267   774 bp   mRNA   linear   EST 20-OCT-2000
   DEFINITION   601432095F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917399 5',
       mRNA sequence.
   ACCESSION   BE891267
   VERSION   BE891267.1 GI:10350429
   KEYWORDS   EST.
   SOURCE   Homo sapiens (human)
   ORGANISM   Homo sapiens
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 774)
   AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
       National Institutes of Health, Mammalian Gene Collection (MGC)
   TITLE   Unpublished (1999)
   JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
       Email: cgapbs-r@mail.nih.gov
       Tissue Procurement: ATCC/DCTD/DTP
       cDNA Library Preparation: Life Technologies, Inc.
       cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
       DNA Sequencing by: Incyte Genomics, Inc.
       Clone distribution: MGC clone distribution information can be
       found through the I.M.A.G.E. Consortium/LLNL at:
       http://image.llnl.gov
       Plate: LLAM9743 row: n column: 24
       High quality sequence stop: 751.
FEATURES   Location/Qualifiers
   source   1..774
       /organism="Homo sapiens"
       /mol_type="mRNA"
       /db_xref="taxon:9606"
       /clone="IMAGE:3917399"
       /tissue_type="melanotic melanoma"
       /lab_host="DH10B (phage-resistant)"
       /clone_lib="NIH_MGC_72"
       /note="Organ: skin; Vector: pCMV-SPORT6; Primer: Oligo dT.
       Site_2: SalI; Cloned unidirectionally. Primer; Oligo dT.
       Average insert size 2 kb. Library constructed by Life
       Technologies."
ORIGIN

US-09-976-740-7 (1-217) x BE891267 (1-774)

Alignment Scores:
Pred. No.:   8.69e-53
Score: 992.00
Percent Similarity: 94.59%
Best Local Similarity: 94.14%
Query Match: 84.79%

Length: 774
Matches: 209
Conservative: 1
Mismatches: 5
Indels: 9
Gaps: 2

Qy   1 GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluAspGluGlu 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   104 GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGAAGATGAAGATGAAGAA 163

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
         |||||||||||||||||||||||||||||||||||||||||||:::||||
Db   164 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGGTCCCAGGAGGGTCCCAGCAC 223

Qy   158 GlnAlaThrAlaPheGlnGluGlnGlnIleAspGlyValLysSerIleLeuLeuMetGlnArg 177
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432 CAGGCCACTGCTTTTCAAGAGCAGCAGATAGACGGAGTCAAAAGTCTTCTGATGCAACGG 491

Qy   178 ThrAspThrLeuThrGlyIleLeuSerIleArgLeuGlyProAlaLeuLysGluLysGlyHis 197
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   492 ACAGATGTGCTCACTGGCATCCATTCGCCTGCGCTGAAGGAGAAGGGTCACAGC 551

Qy   198 HisSerIleLysValLeuGlnIleGlyHisSerPheGluAsnAspAspAspProSerGlyPheLeuGly 217
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552 CACATCAAGGTGCTTCAGCAAGGCCACTTGAGGAATGATGAGATCCTGAGTGGCCTTCTAGGC 611

RESULT 12

```
BI987692
LOCUS       BI987692          600 bp    mRNA    linear    EST 20-DEC-2001
DEFINITION  3204-64 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
ACCESSION   BI987692
VERSION     BI987692.1  GI:17958662
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 600)
AUTHORS     Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE       Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
JOURNAL     Nucleic Acids Res. 29 (24), 4983-4993 (2001)
MEDLINE     21671825
PUBMED      11812828
COMMENT     Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES             Location/Qualifiers
source          1..600
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /tissue_type="neural retina"
                /dev_stage="embryonic day 14.5 post-fertilization"
                /clone_lib="Mouse E14.5 retina lambda ZAP II Library"
ORIGIN
```

Alignment Scores:

```
Pred. No.:              1.14e-52      Length:            600
Score:                   988.00       Matches:           181
Percent Similarity:      95.90%       Conservative:        6
Best Local Similarity:   92.82%       Mismatches:          8
Query Match:             84.44%       Indels:              0
DB:                      12           Gaps:                0
```

US-09-976-740-7 (1-217) x BI987692 (1-600)

```
Qy   41 HisGlnLeuAsnGlyLeuArgGlyLeuProGlnSerAlaLysGluArgGlyValLysGluTrpThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  224 CACCAGCTTAACGGGCCGAGCCGGGGACCTCAGAGTGCCAAGGAGAGGGGTCAAGGAGTGGACC 283

Qy   61 ProCysGlyProHisGlnGlyLeuAspGluGlyArgGlyProAlaProGlySerGlyThr 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  284 CCCTGCGGACCGCACCA-GGCCAGGATGAAGGGCGGCGGCCAGCCCCGGGAGCGGCACC 342

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  343 CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGACGGCTTCGTTGCCACC 402

Qy  101 GlyLeuProAsnSerProSerProAlaProLeuProLeuProAlaLeuProGlyAla 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  403 GGGCCAGACTCCCCGTCCCCCGTGCCCTTGCCCCTAGCCCTTGGGGCC 462

Qy  121 AspGlyThrProPheGlyCysProGlyProGlyValArgGlyLeuLysProSerAspProValGlu 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  463 GACGGGACACCCCTTTGGCTGTCCTCCCGGGCGCGAAAGAGAGCCATCTGATCCCGTCGAG 522

Qy  141 TrpThrValMetAspValValGlu--TyrPheThrGluAla-GlyPhePro---GluGlnA 159
        |||||||||||||||||||||        |||||||||||
Db  523 TGGACCGTGATGGAGGTGTCGTTGAGAAATATTTTACTGAGGCTGGATTTCCCGGGAC 582

Qy  159 laThrAlaPheGlnGluGlnIleLeuAspGlyLysSerLeuLeuLeu--MetGln-ArgTh 178
        |||||||||||||||||||||||||||||||||||||||
Db  583 CGACAGCTTTCCAAGAGCAGGAAAATTGATGGCAAATCTTTGCTGCTCAATGCAGCGCGCAC 642

Qy  178 rAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHi 198
        ||||||||||||||||||||||||||||||||||||||||||
Db  643 AGATGTGCTCACCGGCTTGTCCATCCGCCTGGGCCCAGC-CTGAAAAATCTACGAGCACCA 701

Qy  198 sIleLysValLeuGlnAlnGlyHisPheGluAsp-AspAspProAspGlyPheLeu 216
        |||||||||||||||||||||        ||||||
Db  702 CATCAAGGTGCTTCAGCAG---CCACTTGAGGATTGATGACCCCGATGGGTTCTTA 754
```

US-09-976-740-7 (1-217) x BE270987 (1-600)

```
Pred. No.:              1.14e-52      Length:            600
Score:                   988.00       Matches:           181
Percent Similarity:      95.90%       Conservative:        6
Best Local Similarity:   92.82%       Mismatches:          8
Query Match:             84.44%       Indels:              0
                                      Gaps:                0
```

RESULT 13

```
BE270987/c
LOCUS       BE270987/c        829 bp    mRNA    linear    EST 13-JUL-2000
DEFINITION  601094380471 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966449 3',
            mRNA sequence.
ACCESSION   BE270987
VERSION     BE270987.1  GI:9144634
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 829)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
```

```
Qy   23 ValSerGluGluGlyGluValValProGluSerArgProAlaGlyAlaGlyHisHisGln 42
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3 GTATCTGAGGGGCTCAGAAGTGCCCGGAGAGTGACCGCCCCCAGCAGGTGCTCAGCACCATCAG 62

Qy   43 LeuAsnGlyLeuArgGlyLeuProGlnSerAlaLysGluArgGlyValLysGluTrpThrProCys 62
        :::||||||||||||||||||||||||||||||||||||||||||||||||::::||||
Db   63 ATTAATGGAGAGCCGGGGGGCTCAGAGTGCTAAGGAGAGGGTCAAGGAGTGGCTCGCCCCTGT 122

Qy   63 GlyProHisGlnGlyLeuAspGluGlyArgGlyProAlaProGlySerGlyThrArgGln 82
        ||||||:::||||||||||||||||||||||||||||||::::||||||
Db  123 GGACCCTACCAGGCCAGGATGAAGGGCGGCGGCCAGCCCTGCACACGGCAGCAG 182

Qy   83 ValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThrGlyLeuPro 102
        |||||||||||||||||||||||||||::::|||||||||||||||||||||
Db  183 GTGTTCCCGATGACAGCTGTGAATAAAGAAGGGGGATCAGCTTGTGTTGGAGCAGCTCCA 242

Qy  103 AspSerProSerProAlaProLeuProLeuProAlaLeuProGlyAlaAspGly 122
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  243 GATTCTCCANCTCCGGCCCTTGCCTTGCCCTCCAGGAAAACCAGCTTACGAGGTCGATTGGG 302

Qy  123 ThrProPheGlyCysProGlyProGlyValArgGlyLeuLysProSerAspProValGluTrpThr 142
        ||||||||||||||||||||||||||||::::||||||||||||||||||||
Db  303 ACACCTTTTGGCTGTCCTCCCGGTCCCCCGGGCGGGAAGGAGAGCACCCAGTGGAGTGGACA 362

Qy  143 ValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPhe 162
        |||||||||||||||||::::||||||||||::::|||||||||||
Db  363 GTCCATGGATGTGGGTGGGAATACTTCACTGAGGCGGGGCCTTCCCAGGAGCAGCCCACTGCTTTT 422

Qy  163 GlnGluGlnIleLeuAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThr 182
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  423 CAAGGAGCAGGAAAATTGATGGCAAGTCTTTGTTGCTCATGCAACGGACAGCAGATGTGCTCACT 482

Qy  183 GlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeu 202
        |||||||||||||||||||||||||||||||||||||||||
Db  483 GGCCTATCCATCCGCCTGGGCCCAGCCCTGAAGATCTACGAGCACCACATCAAGGTGCTT 542

Qy  203 GlnAlaGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217
        ||||||||||||||||||||||||||||||||||||
Db  543 CAGCAAGGCCACTTTGAGGATGATGAATCCTGATGGCCTTCTAGGC 587
```

Plate: LLCM69   row: h   column: 02
High quality sequence start: 26
High quality sequence stop: 773.

FEATURES   Location/Qualifiers
source   1..829
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:2966449"
   /tissue_type="Burkitt lymphoma"
   /lab_host="DH10B (phage-resistant)"
   /clone_lib="NIH_MGC_8"
   /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
   EcoRI; cDNA made by oligo-dT priming. Directionally
   cloned into EcoRI/XhoI sites using the following 5'
   adaptor: GGCACGAG (G). Size-selected >500bp for average
   insert size 1.8kb. Library constructed by Ling Hong in
   the laboratory of Gerald M. Rubin (University of
   California, Berkeley) using ZAP-cDNA synthesis kit
   (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

US-09-976-740-7 (1-217) x BE270987 (1-829)

Alignment Scores:
Pred. No.:   1..946-52
Score: 987.00
Percent Similarity: 96.63%
Best Local Similarity: 94.23%
Query Match: 84.36%
DB: 10

		Length:	829
		Matches:	196
		Conservative:	5
		Mismatches:	5
		Indels:	4
		Gaps:	0

```
Qy   11 GluAspAspAspGluAspGluAspGluAlaSerGluGlyGlySerGluValPr  30
           ||||||||||||||||||||  ::|||||||||||||||||||||||||
Db  829 GAAGATGATGAAGAAGGAGAAGAAGGAGAAGAAGAGATGAATGTTCAGAAGGGTTCTGAAAGGCC  770

Qy   30 oGluSerAspArgProAlaGlyValAlaGlnHisHisGlnLeuAsnGlyGluArgGlyProGl  50
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  769 CGAGAGTGACGTCCTGCAGGGCC--CAGCACCACCAGCT--AACCGCGACCGGGGACCTCA  712

Qy   50 nSerAlaLysGluArgValLysGluTrpThrProCysGlyProHisGlnGlyGlnAspGl  70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  711 GAGTGCCAAGGAGAGGTC-AAGGAGTGGACCCCGTGCGGACCCCACCAGGGCCAGGAGATGA  653

Qy   70 uGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAs  90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  652 AGGGCGGGGACCAGCCCCCGGCAGCGGGACCCGGCCGTGTTCTTCCATGGCAGCCATGAA  593

Qy   90 nLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerProValProLe  110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  592 CAAGGAAGGGGGAACAGCTTCTGTTGCCACCGGCCAGACTCCCGTCCCCGTGCCTTT  533

Qy  110 uProGlyLysProGlyValAlaLeuProGlyValAlaAspGlyThrProPheGlyCysProProGl  130
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  532 GCCCCCAGGGCCAAACCAGCCCTACCTGGGCGGGCGGGACCCCTTGGCTGTCCTCCGG  473

Qy  130 yArgGlyLysGlyLysProSerAspProValGluTrpThrValMetAspValValGluTyrPh  150
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  472 GCGCAAAGAGAAGCCATCTGAATCCGTCGACCCGTGAGTGGACTGGTGCATGGTGGAATATTT  413

Qy  150 eThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGlnGlnGlnIleAspGlyLy  170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  412 TACTGAGGCTGGATTCCCGGAGCAGGCCACAGCTTTCCAAGAGCAGGAAATTGATGGCAA  353

Qy  170 sSerLeuLeuLeuMetGlnArgThrAspValLeuSerIleArgLeuGlyPr  190
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 ATCTTTGCTGCTCATGCAGCGCACAGATGTCCTCAGCATCCGCCTCCGGCC  293

Qy  190 oAlaLeuLysIleTyrGluHisHisHisLysLysValLeuGlnGlyHisPheGluAspAs  210
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 AGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTTGAGGATGA  233

Qy  210 pAspProAspGlyPheLeuGly  217
           ||||||||||||||||||||||
Db  233                         217
```

Db   232   TGACCCGATGGCTTCTTAGGC   211

RESULT 14
BF058975
LOCUS   BF058975   704 bp   mRNA   linear   EST 16-OCT-2000
DEFINITION   7k36f08.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3477639 3'
   similar to TR:O76865 O76866 EG:100G10.6 PROTEIN. [1] ;contains
   element MER22 repetitive element i; mRNA sequence.
ACCESSION   BF058975
VERSION   BF058975.1   GI:10812871
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 704)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
   Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
   R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
   Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
   I.M.A.G.E. Consortium DNA Sequencing by: Washington University
   Genome Sequencing Center
   Clone distribution: NCI-CGAP clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL. send email to:
   info@image.llnl.gov

FEATURES   Location/Qualifiers
source   1..704
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:3477639"
   /tissue_type="fibrotheoma"
   /lab_host="DH10B (phage-resistant)"
   /clone_lib="NCI_CGAP_Ov18"
   /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
   modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
   strand cDNA was primed with a Not I - oligo(dT) primer [5'
   TGTTACCAATCTGAAGTGGGAGCGGGCGGCGGGCGGTTTTTTTTTTTTTTTTTT 3'];
   double-stranded cDNA was ligated to Eco RI adaptors
   (Pharmacia), digested with Not I and cloned into the Not
   I and Eco RI sites of the modified pT7T3 vector. Library
   went through one round of normalization, and was
   constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-7 (1-217) x BF058975 (1-704)

Alignment Scores:
Pred. No.:   2.15e-51
Score: 969.00
Percent Similarity: 98.91%
Best Local Similarity: 98.36%
Query Match: 82.82%
DB: 10

		Length:	704
		Matches:	180
		Conservative:	1
		Mismatches:	2
		Indels:	0
		Gaps:	0

```
Qy    1 GluGluArgValLeuGluLysGluLeuGluGluAspAspAspGluAspGluAspGluGlu  20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  156 GAAGACGGAGTACTTGAAGAAAGAGAAGAGAAGAAGATGATGAAGATGAAGATGAAGAAGAA  215

Qy   21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis  40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  216 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTCGCAGGTGCCCAGCAC  275

Qy   41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db                                                                60
```

```
Alignment Scores:
Pred. No.:
Score:                  2.37e-51
Percent Similarity:     967.00
Best Local Similarity:  96.00%
Query Match:            89.50%
DB:                     82.65%
                        12

Length:                 600
Matches:                179
Conservative:           13
Mismatches:             7
Indels:                 1
Gaps:                   0
```

```
ORIGIN

FEATURES             Location/Qualifiers
     source          1..600
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="neural retina"
                     /dev_stage="embryonic day 14.5 post-fertilization"
                     /clone_lib="Mouse E14.5 retina lambda ZAP II Library"

COMMENT     Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
  TITLE     Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
  JOURNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
   MEDLINE  21671825
   PUBMED   11812828
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SOURCE      Mus musculus (house mouse)
KEYWORDS    EST.
VERSION     BI985158.1  GI:17956088
ACCESSION   BI985158
DEFINITION  3132-24 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
LOCUS       BI985158    600 bp    mRNA    linear    EST 20-DEC-2001
```

```
RESULT 15
```

```
Db  276 CACCAGCTTAACGCCGACGCGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 335

Qy   61 ProCysGlyTyrProHisGlnIleGlyThrGlyTyrAspGluGlyArgGlyTyrProAlaProGlySerGlyThr 80

Db  336 CCTGCGACGACCACCAGGGCCCAGGATGAAGAGGGCGGGGCCAGGCACCAGGCACCACC 395

Qy   81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlyLeuGlyGlyTyrAlaSerValAlaThr 100

Db  396 CGCCAGGGTGTTCTCCATGGCGGCCATGAACAAGGGAAGAGGCGGGTTCGCCACC 455

Qy  101 GlyTyrProAspSerProSerProValProLeuProProGlyTyrLysProAlaLeuProGlyAla 120

Db  456 GGGGCCAGACTCCCCGTCCCCCCGTGCCCCAGGCAAACCAGCCCTACCTGGGGGCC 515

Qy  121 AspGlyThrProPheGlyCysProProGlyTyrArgLysGlyLysProSerAspProValGlu 140

Db  516 GACGGGACACCCCTTNTGGCGTCCTCCCGGGCGCGCAAAGAGAAGCCATCTGANTCCCGTCGAG 575

Qy  141 TrpThrValMetAspValValGluTyrPheThrGluGlnGlnIleAlaThr 160

Db  576 TGGACCGTGATGGATGTCGTGGAATATTTNTACTGAATTCCCGGAGCAGCAGATTGCAACT 635

Qy  161 AlaPheGlnGluGlnGlnIleLeuAspProGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180

Db  636 GCTTTCCAAGAGCAGCAGAAAATTGATGGCCAAATCTTTGCTGCTCATGCAGCGGACAGATGTG 695

Qy  181 LeuThrGly 183
         |||||||||
Db  696 CTCACCGGG 704
```

```
US-09-976-740-7 (1-217) x BI985158 (1-600)

Qy    6 GlyLysGlyGluGluGluAspAspAspGluAspGluGluGlnGlnGln 25
         |||:||||||||||||||||||:||||||
Db    2 AAAGAAGAGGAAGATGAGGAATGAAGACGAGGAGGAGGAGCAAATGTATCTGAG 61

Qy   26 GlySerGluLeuProGlyGluSerAspArgProAlaGlyValAlaGlyGlnHisHisGlnLeuAsnGly 45
         |||:|||||||||||||||||||||||||:||
Db   62 GGCTCAGAGAGTGCCCGAGAGTGACCGCCCCGCCGGAGGTGCTGCAGCACCATCAGATTAATGGA 121

Qy   46 GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProProCysGlyTyrProHis 65
         |||||||||||||:||||||||||||:|||||
Db  122 GAGCGGGGGCCCTCAGAGTGCTTAAGGAGGAGGGTCAAGGAGTGGACCCCTAC 181

Qy   66 GlnGlyGlyAspGlyTyrArgGlyTyrProAlaProGlySerGlyThrArgGlnValPheSer 85
         ||||||||||||||||||||||||||||||||
Db  182 CAGGGCGGAGATGAGGGGCGGGGGACCAGGCAGGTGTTCCCG 241

Qy   86 MetAlaAlaMetAsnLysGlyLeuGlyGlyTyrAlaSerValAlaThrGlyTyrProAspSerPro 105
         |||||||||||||||||||||||||||||:||
Db  242 ATGACAGCTGTGAATAAAGGAAGAGGGGGATCAGCTTGTGGAGCTCCAGATTCTCCA 301

Qy  106 SerProValProLeuProProGlyTyrLysProAlaLeuProGlyAlaAspGlyThrProPhe 125
         ||||||||||||||||||||||||:||||||
Db  302 TCTCCGGTGCCTTTGCCCTCCAGGAAAACCAGCCCTACCTGGGGGTGGATGGAACCTTT 361

Qy  126 GlyCysProProGlyTyrArgLysGlyLysProSerSerAspProValGluTrpThrValMetAsp 145
         |||||||||||||||||||||||||:|||||
Db  362 GGCTGTCCTCCCGGGCGCAAGGAGAAGCCGACACGACAGTGGGATG 421

Qy  146 ValValGluTyrPheThrGluGlnGlnIleAlaThrAlaPheGlnGluGln 165
         ||||||||||||||||||||||||:|||||
Db  422 GTGGTGGAATACTTCACTGAGCGGCGGTCTCCCAGCAGAGCAG 481

Qy  166 GlnIleLeuAspProGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 185
         |||||||||||||||||||||||||||||||
Db  482 GAAATTGATGGCAAGTCTTTGTTGCTCATGCAACGGACAGATGTGCTCACTGGCCTATCC 541

Qy  186 IleArgLeuGlyProAla-LeuLysSerIleTyrGluHisSerIleLeuLysSerValLeuGluGlnGln 204
         ||||||:||||||||||::|||||
Db  542 ATCCGCCTGGGCCCAGCCCCTGAAGATCTACGAGCACAGCATCAGAAGGTGCTTCAGCAA 599
```

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 227.827 Seconds
             (without alignments)
             2853.675 Million cell updates/sec

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2004 Compugen Ltd.

Title:
Perfect score: 82
Sequence: US-09-976-740-19

Scoring table: 1 EEEEDDDEDEDEEDD 15

                BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext 7.0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched: 3470272 seqs, 2167:516995 residues

Total number of hits satisfying chosen parameters: 6940544

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_b/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US09976740 @CGN_1_1_9705 @runat_10032004_094548_19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -YGAPOP=10 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
 1:   gb_ba:*
 2:   gb_bg:*
 3:   gb_in:*
 4:   gb_om:*
 5:   gb_ov:*
 6:   gb_pat:*
 7:   gb_ph:*
 8:   gb_pl:*
 9:   gb_pr:*
10:   gb_ro:*
11:   gb_sts:*
12:   gb_sy:*
13:   gb_un:*
14:   gb_vi:*
15:   em_ba:*
16:   em_fun:*
17:   em_hum:*
18:   em_in:*
19:   em_mu:*
20:   em_Om:*
21:   em_or:*
22:   em_ov:*
23:   em_pat:*
24:   em_ph:*
25:   em_pl:*
26:   em_ro:*
27:   em_sts:*
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	45	6	AR199538	AR199538 Sequence
2	82	100.0	45	6	AR374690	AR374690 Sequence
3	82	100.0	45	6	AR409325	AR409325 Sequence
4	82	100.0	45	6	AX239587	AX239587 Sequence
5	82	100.0	45	6	BD056452	BD056452 Novel low
6	82	100.0	78	6	AR199539	AR199539 Sequence
7	82	100.0	78	6	AR374691	AR374691 Sequence
8	82	100.0	78	6	AR409326	AR409326 Sequence
9	82	100.0	78	6	AX239588	AX239588 Sequence
10	82	100.0	982	9	BD056453	BD056453 Novel low
11	82	100.0	1208	6	BC007384	BC007384 Homo sapi
12	82	100.0	1208	6	AR199535	AR199535 Sequence
13	82	100.0	1208	6	AR374687	AR374687 Sequence
14	82	100.0	1208	6	AR409322	AR409322 Sequence
15	82	100.0	1208	6	AX239573	AX239573 Sequence
16	82	100.0	1470	6	BD056449	BD056449 Novel low
17	82	100.0	1614	6	BC030129	BC030129 Homo sapi
18	82	100.0	1614	6	AR409337	AR409337 Sequence
19	82	100.0	1614	6	AX239602	AX239602 Sequence
20	82	100.0	1617	9	AY453840	AY453840 Homo sapi
21	82	100.0	12425	6	AR409341	AR409341 Sequence
22	82	100.0	12425	6	AX239607	AX239607 Sequence
23	82	100.0	237931	4	AC022098	AC022098 Homo sapi
24	79	96.3	1521	5	OAU35655	OAU35655 Sequence
25	76	92.7	335	5	PFL538319	PFL538319 Platichth
26	76	92.7	29150	3	AJ115683	AJ115683 Dictyoste
27	75	91.5	1442	8	L38856	L38856 Glycine max
28	75	91.5	152564	10	AC127549	AC127549 Mus muscu
29	75	91.5	177408	2	AC115847	AC115847 Mus muscu
30	75	91.5	233181	2	AC111558	AC111558 Rattus no
31	74	90.2	1249	10	BC019416	BC019416 Mus muscu
32	74	90.2	2576	5	GGNUCC23	GGNUCC23 Chicken mRN
33	74	90.2	3452	5	D88440	D88440 Gallus gall
34	74	90.2	12028	2	AE001412	AE001412 Plasmodiu
35	74	90.2	68671	2	AC101600	AC101600 Mus muscu
36	74	90.2	110000	2	BX571702_2	BX571702_2 Continuation (3 of
37	74	90.2	169094	10	AC129013	AC129013 Mus muscu
38	74	90.2	172611	2	AC121664	AC121664 Rattus no
39	74	90.2	197650	2	AC107704	AC107704 Mus muscu
40	74	90.2	204911	10	AC109169	AC109169 Mus muscu
41	74	90.2	213739	2	AC113937	AC113937 Mus muscu
42	74	90.2	217932	2	AC115817	AC115817 Mus muscu
43	74	90.2	220554	2	AC111211	AC111211 Rattus no
44	74	90.2	223318	10	BX284111	BX284111 Mouse DNA
45	74	90.2	239824	2	AC121166	AC121166 Rattus no

RESULT 1

ALIGNMENTS

AR199538
LOCUS   AR199538   45 bp   DNA   linear   PAT 20-APR-2002
DEFINITION   Sequence 30 from patent US 6355451.
ACCESSION   AR199538
VERSION   AR199538.1 GI:20249612
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 45)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 30 12-MAR-2002;
FEATURES   Location/Qualifiers
  source   1..45
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Qy US-09-976-740-19 (1-15) x AR199538 (1-45)

Qy 1 GluGluGluGluAspProAspGluAspProGluGluAspProGluGluAspAsp 15
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 45

RESULT 2
LOCUS   AR374690   45 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION   Sequence 30 from patent US 6605588.
ACCESSION   AR374690
VERSION   AR374690.1 GI:40077505
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 45)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 30 12-AUG-2003;
FEATURES   Location/Qualifiers
  source   1..45
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Qy US-09-976-740-19 (1-15) x AR374690 (1-45)

Alignment Scores:
Pred. No.:
Score: 0.000235
Percent Similarity: 82.00   Length: 45
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
                         6   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

Qy 1 GluGluGluGluAspProAspGluAspProGluGluAspProGluGluAspAsp 15
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 45

RESULT 3
LOCUS   AR409325
DEFINITION   Sequence 30 from patent US 6632923.

ACCESSION   AR409325
VERSION   AR409325.1 GI:40160113
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 45)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 30 14-OCT-2003;
FEATURES   Location/Qualifiers
  source   1..45
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Qy US-09-976-740-19 (1-15) x AR409325 (1-45)

Qy 1 GluGluGluGluAspProAspGluAspProGluGluAspProGluGluAspAsp 15
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 45

RESULT 4
LOCUS   AX239587   45 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION   Sequence 30 from Patent WO0164874.
ACCESSION   AX239587
VERSION   AX239587.1 GI:15797263
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 45)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
             and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 30 07-SEP-2001;
             Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
  source   1..45
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Qy US-09-976-740-19 (1-15) x AX239587 (1-45)

Alignment Scores:
Pred. No.:
Score: 0.000235
Percent Similarity: 82.00   Length: 45
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
                         6   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

Qy 1 GluGluGluGluAspProAspGluAspProGluGluAspProGluGluAspAsp 15
       ||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 45

RESULT 5
LOCUS   BD056452
DEFINITION   Novel low density lipoprotein binding proteins and their use in

diagnosing and treating atherosclerosis,.

ACCESSION   BD056452
VERSION   BD056452.1 GI:22602058
KEYWORDS   JP 200150698-A/10.
SOURCE   Aequorea victoria
  ORGANISM   Aequorea victoria
             Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
             Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 45)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 200150698-A 10 29-MAY-2001;
             BOSTON HEART FOUNDATION INC
COMMENT   PN JP 200150698-A/10
             PD 29-MAY-2001
             PF 26-NOV-1997 JP 1998524870
             PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
             ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
             A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
             C07H21/00,
             PC C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
             CC Strandedness: Single;
             CC Topology: Linear;
             FH Key   Location/Qualifiers
FEATURES
     source   1..45
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.000235   Length: 45
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                                               Indels: 0
                                               Gaps: 0

US-09-976-740-19 (1-15) x BD056452 (1-45)

Qy 1 GluGluGluGluAspAspAspGluAspGlyGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAT 45

RESULT 6
AR199539
Db
LOCUS   AR199539   78 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 31 from patent US 6355451.
ACCESSION   AR199539
VERSION   AR199539.1 GI:20249613
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 31 12-MAR-2002;
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.000399   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                                               Indels: 0

DB: 6   Gaps: 0

US-09-976-740-19 (1-15) x AR199539 (1-78)

Qy 1 GluGluGluGluAspAspAspGluAspGlyGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGAAGATGAT 45

RESULT 7
AR374691
Db
LOCUS   AR374691   78 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 31 from patent US 6605588.
ACCESSION   AR374691
VERSION   AR374691.1 GI:40077506
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 31 12-AUG-2003;
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.000399   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                                               Indels: 0
                                               Gaps: 0

US-09-976-740-19 (1-15) x AR374691 (1-78)

Qy 1 GluGluGluGluAspAspAspGluAspGlyGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAT 45

RESULT 8
AR409326
Db
LOCUS   AR409326   78 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 31 from patent US 6632923.
ACCESSION   AR409326
VERSION   AR409326.1 GI:40160114
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 31 14-OCT-2003;
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.000399   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                                               Indels: 0
                                               Gaps: 0

US-09-976-740-19 (1-15) x AR409326 (1-78)

Qy 1 GluGluGluGluAspAspAspGluAspGlyGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAT 45

Qy   1 GluGluGluGluAspAspAspGluGluAspGluGluAspAsp 15
Db   1 GAAGAGGAAGAAGATGATGATGAAGAGATGAAGAGAGATGAT 45

```
Qy      1 GluGluGluGluAspAspAspGluGluAspGluGluAspAsp 15
```

RESULT 9
LOCUS   AX239588
DEFINITION   AX239588
DEFINITION   Sequence 31 from Patent WO0164874.
ACCESSION   AX239588
VERSION   AX239588.1 GI:15797264
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
             and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 31 07-SEP-2001;
             Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..78
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.000399
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

US-09-976-740-19 (1-15) x AX239588 (1-78)

Qy   1 GluGluGluGluAspAspAspGluGluAspGluGluAspAsp 15
Db   1 GAAGAGGAAGAAGATGATGATGAAGAGATGAAGAGAGATGAT 45

RESULT 10
LOCUS   BD056453   78 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   BD056453
DEFINITION   Novel low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis.
ACCESSION   BD056453
VERSION   BD056453.1 GI:22602059
KEYWORDS   JP 2001506983-A/11.
SOURCE   Aequorea victoria
  ORGANISM   Aequorea victoria
             Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
             Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 11 29-MAY-2001;
             BOSTON HEART FOUNDATION INC
COMMENT   PN   JP 2001506983-A/11
             PD   29-MAY-2001
             PF   26-NOV-1997 JP 199852487O
             PR   27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI
             ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
             A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
             C07H21/00,
             PC C07K7/00,C07K14/705,C12N15/12,C12O1/02,C12O1/68,G01N33/566 CC
             Strandedness: Single;
             CC   Topology: Linear;
FEATURES   FH   Key   Location/Qualifiers
                  Location/Qualifiers.
```

ORIGIN

source   1..78
                /organism="Aequorea victoria"
                /mol_type="genomic DNA"
                /db_xref="taxon:6100"

US-09-976-740-19 (1-15) x BD056453 (1-78)

Qy   1 GluGluGluGluAspAspAspGluGluAspGluGluAspAsp 15
Db   1 GAAGAGGAAGAAGATGATGATGAAGAGATGAAGAGAGATGAT 45

Alignment Scores:
Pred. No.:
Score: 0.000399
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

RESULT 11
LOCUS   BC007384   982 bp   mRNA   linear   PRI 16-SEP-2003
DEFINITION   BC007384
DEFINITION   Homo sapiens hypothetical protein BC007384, partial cds.
ACCESSION   BC007384
VERSION   BC007384.2 GI:33988219
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 982)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
             McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
             Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
             Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
             Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
             Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
             Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2 (bases 1 to 982)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (01-MAY-2001) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   On Aug 20, 2003 this sequence version replaced gi:13938477.
             Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Rubin Library
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Institute for Systems Biology
             http://www.systemsbiology.org
             contact: amadan@systemsbiology.org

REFERENCE
AUTHORS   Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
          Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES
source   Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 24 Row: 9 Column: 10.
          Location/Qualifiers
          1. .982
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="IMAGE:3677194"
          /clone_lib="NIH_MGC_8"
          /tissue_type="Lymph, Burkitt lymphoma"
          /lab_host="DH10B-R"
          /note="Vector: pOTB7"

gene   <1. .982
          /gene="LOC90378"
          /db_xref="LocusID:90378"

CDS   <1. .711
          /gene="LOC90378"
          /codon_start=1
          /product="LOC90378 protein"
          /protein_id="AAH07384.2"
          /db_xref="GI:33988220"
          /db_xref="LocusID:90378"
          /translation="PGRAPPAAAARPSRSKRGGEERVLEKEEEEDDEDEDEEDDVSE
          GSEVPESDRPAGAQHHQLNGERGEQSAKERVKEWTPCGPHQGQDEGRGPAPGSGTRQV
          PSMAAMNKEGGTASVATGPDSPSPVPLPPGKPALPGADGTPFGCPGRKEKPSDPVEW
          TVMDVVEYPTEAGPPEQATAFQEEIDGKSLILMQRDVLIGLSIRLGPALKIYEHHI
          KVLQQGHFEDDDPDGFLG"

misc_feature 469. .669
          /gene="LOC90378"
          /note="SAM; Region: Sterile alpha motif. Widespread domain
          in signalling and nuclear proteins. In EPH-related
          tyrosine kinases, appears to mediate cell-cell initiated
          signal transduction via the binding of SH2-containing
          proteins to a conserved tyrosine that is phosphorylated.
          In many cases mediates homodimerisation"
          /db_xref="CDD:smart00454"

ORIGIN

US-09-976-740-19 (1-15) x BC007384 (1-982)

Qy   1 GluGluGluGluAspAspProGluAspGluAspGluGluAspAsp 15
        |||||||||||||||
Db   79 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAGGAAGATGAT 123

Alignment Scores:
Pred. No.:
Score: 0.00456
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 9
                            Length: 982
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

RESULT 12
LOCUS   AR199535   1208 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 16 from patent US 6355451.
ACCESSION   AR199535
VERSION   AR199535.1 GI:20249609
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
JOURNAL   Patent: US 6355451-A 16 12-MAR-2002;
FEATURES   Location/Qualifiers
source   1. .1208

ORIGIN
          /organism="unknown"
          /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:
Score: 0.00557
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 6
                            Length: 1208
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

US-09-976-740-19 (1-15) x AR199535 (1-1208)

Qy   1 GluGluGluGluAspAspProGluAspGluAspGluGluAspAsp 15
        |||||||||||||||
Db   22 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAGGAAGATGAT 66

RESULT 13
LOCUS   AR374687   1208 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6605588.
ACCESSION   AR374687
VERSION   AR374687.1 GI:40077502
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
JOURNAL   Patent: US 6605588-A 16 12-AUG-2003;
FEATURES   Location/Qualifiers
source   1. .1208
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:
Score: 0.00557
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 6
                            Length: 1208
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

US-09-976-740-19 (1-15) x AR374687 (1-1208)

Qy   1 GluGluGluGluAspAspProGluAspGluAspGluGluAspAsp 15
        |||||||||||||||
Db   22 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAGGAAGATGAT 66

RESULT 14
LOCUS   AR409322   1208 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6632923.
ACCESSION   AR409322
VERSION   AR409322.1 GI:40160110
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1208)
AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
JOURNAL   Patent: US 6632923-A 16 14-OCT-2003;
FEATURES   Location/Qualifiers
source   1. .1208
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN

```
Alignment Scores:
Pred. No.:                            0.00557
Score:                                82.00
Percent Similarity:                   100.00%          Matches:             15
Best Local Similarity:                100.00%          Conservative:         0
Query Match:                          100.00%          Mismatches:           0
DB:                                                    Indels:               0
                                                       Gaps:                 0

Qy        US-09-976-740-19 (1-15) x AR409322 (1-1208)

Qy        1 GluGluGluGluAspAspAspGluAspGluAspGluuAspGluGluAspAsp 15
            |||||||||||||||||||||||||||||||||||||||||||||
Db       22 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAAGATGAAGAAGATGAT 66

RESULT 15
AX239573
LOCUS          AX239573         1208 bp      DNA      linear   PAT 26-SEP-2001
DEFINITION     Sequence 16 from Patent WO0164874.
ACCESSION      AX239573
VERSION        AX239573.1    GI:15797257
KEYWORDS
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
  AUTHORS      Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE        Low density lipoprotein binding proteins and their use in diagnosing
               and treating atherosclerosis
  JOURNAL      Patent: WO 0164874-A 16 07-SEP-2001;
               Boston Heart Foundation, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             <1..654
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC88296.1"
                     /db_xref="GI:15797258"
                     /db_xref="REMTREMBL:CAC88296"
                     /translation="EERVLEKEEEDDEDEDEEDDVSEGSEVPESDRPAGAQHHQLN
                     GERGPQSAKERVKEWTPCGPHQGQDERGPAPGSGTRQVFSMAANKEGGTASVAIGP
                     DSPSPVPLPPGKPALPGADGTPPGCPPGRKEKPSDPVEWTVMDVEYFTEAGFPEQAT
                     AFQEQEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHIKVLQQGHFEDDDPDGFLG"

ORIGIN

Alignment Scores:
Pred. No.:                            0.00557
Score:                                82.00
Percent Similarity:                   100.00%          Length:             1208
Best Local Similarity:                100.00%          Matches:              15
Query Match:                          100.00%          Conservative:          0
DB:                                                    Mismatches:            0
                                                       Indels:                0
                                                       Gaps:                  0

Qy        US-09-976-740-19 (1-15) x AX239573 (1-1208)

Qy        1 GluGluGluGluAspAspAspGluAspGluuAspGluGluAspAsp 15
            |||||||||||||||||||||||||||||||||||||||||||||
Db       22 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAAGATGAAGAAGATGAT 66

Search completed: March 13, 2004, 00:35:24
Job time : 231.827 secs
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:48:14 ; Search time 23.776 Seconds
(without alignments)
2680.137 Million cell updates/sec

Title: US-09-976-740-19
Perfect score: 82
Sequence: 1 EEEEDDDEDEDEED 15

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 212409041 residues
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Command line parameters:
-MODEL=frame+ p2n.model -DEV=~lp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-D=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN_1_1_1596 @runat_10032004_094547_19532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	82	100.0	45	5	AAH26502	Low densi
	2	82	100.0	78	5	AAH26503	Low densi
	3	82	100.0	1208	2	AAV32838	Human low
	4	82	100.0	1208	5	AAH26494	Human low
	5	82	100.0	1336	3	AAF21860	Human bre
	6	82	100.0	1614	5	AAH26499	Human low
c	7	82	100.0	12425	3	AAH26495	Human low
c	8	74	90.2	2919	3	AAA70216	Plasmodiu
	9	73	89.0	2044	3	AAZ43754	Murine NN
	10	73	89.0	4599	2	AAT27052	RRP3 telo
	11	72	87.8	643	3	AAC44095	Arabidops
	12	72	87.8	872	6	ABN98791	Arabidops
	13	72	87.8	893	6	AAC42206	Arabidops
	14	72	87.8	1284	6	ABZ32099	Candida a
	15	72	87.8	15790	6	ABQ76615	C. albica
	16	72	87.8	24142	6	ABQ76613	C. albica
c	17	72	87.8	454	6	ABL63824	Breast ca
c	18	71	86.6	454	2	ABN95965	Gene #246
c	19	71	86.6	833	2	AAX39730	Gastric c
	20	71	86.6	1007	7	AAX39731	Gastric c
	21	71	86.6	1962	7	ABQ77438	Human CGD
	22	71	86.6	2142	7	ABK63660	Rat seque
	23	71	86.6	2142	7	ABT41831	Toxicity
	24	71	86.6	2142	9	ADB58108	Toxicity-
	25	71	86.6	2142	9	ADB52591	Primary r
	26	71	86.6	2463	9	ADD89111	Encoding
	27	71	86.6	2495	4	ABL14237	Drosophil
	28	71	86.6	2736	4	ABK84322	Human CDN
	29	71	86.6	2736	9	ABJ31350	Bicalutam
	30	71	86.6	2824	7	ABQ77434	Human CGD
	31	71	86.6	2906	7	ABQ77440	Human CGD
	32	71	86.6	3005	7	ABQ77439	Human CGD
	33	71	86.6	4167	4	ABL21708	Drosophil
	34	71	86.6	5402	4	ABL14236	Drosophil
	35	71	86.6	7585	2	AAV68403	Human BAZ
	36	71	86.6	7585	2	ACF34516	Gene enco
	37	70	85.4	190	3	AAC07764	Human sec
	38	70	85.4	402	2	AAT20520	Human gen
	39	70	85.4	430	9	ADD49446	Human lun
	40	70	85.4	434	4	AAS58740	cDNA #141
	41	70	85.4	443	9	ADD32972	Human mit
	42	70	85.4	459	7	ABX35754	Bovine ES
	43	70	85.4	576	5	AAS84117	DNA encod
	44	70	85.4	592	5	ABV44417	Human pro
	45	70	85.4	703	6	ABS77067	Frog embr

ALIGNMENTS

RESULT 1
AAH26502
ID AAH26502 standard; DNA; 45 BP.
XX
AC AAH26502;
XX
DT 12-NOV-2001 (first entry)
XX
DE Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS Mammalia.
XX
PN WO200164874-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-0051784 9.
PR 14-JUL-2000; 2000US-0061628 9.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR WPI; 2001-565505/63.
XX
PT New isolated low density lipoprotein binding polypeptide for treating,
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

```
XX
PS   Disclosure; Page 9; 143pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB2797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, and methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 45 BP; 22 A; 0 C; 16 G; 7 T; 0 U; 0 Other;

US-09-976-740-19 (1-15) x AAH26502 (1-45)

Qy     1 GluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||||||||
Db     1 GAAGAGGAAGAAGATGATGATGATGAAGATGAAGAAGATGAT 45

Alignment Scores:
Pred. No.:
Score:                    0.000369     Length:        45
                          82.00        Matches:       15
Percent Similarity:       100.00%      Conservative:   0
Best Local Similarity:    100.00%      Mismatches:     0
Query Match:              100.00%      Indels:         0
DB:                       5            Gaps:           0

RESULT 2
AAH26503
ID   AAH26503 standard; DNA; 78 BP.
AC   AAH26503;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS   Mammalia.
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784;
PR   14-JUL-2000; 2000US-0061628.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
     Disclosure; Page 9; 143pp; English.

XX
PS   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB2797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, and methods for evaluating an agent
```

```
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 78 BP; 29 A; 7 C; 29 G; 13 T; 0 U; 0 Other;

US-09-976-740-19 (1-15) x AAH26503 (1-78)

Qy     1 GluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||||||||
Db     1 GAAGAGGAAGAAGATGATGATGATGAAGATGAAGAAGATGAT 45

Alignment Scores:
Pred. No.:
Score:                    0.000624     Length:        78
                          82.00        Matches:       15
Percent Similarity:       100.00%      Conservative:   0
Best Local Similarity:    100.00%      Mismatches:     0
Query Match:              100.00%      Indels:         0
DB:                       5            Gaps:           0

RESULT 3
AAV32838
ID   AAV32838 standard; cDNA; 1208 BP.
AC   AAV32838;
XX
DT   09-NOV-1998   (first entry)
XX
DE   Human low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2;
KW   receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key                Location/Qualifiers
FT   CDS                1..654
FT   misc_feature       22..99
FT                      /tag= a
FT   misc_feature       22..66
FT                      /tag= c
FT                      /note= "Claim 13"
FT   misc_feature       67..99
FT                      /tag= b
FT                      /note= "Claim 12"
FT   misc_feature       
FT                      /tag= d
FT                      /note= "Claim 14"
FT   misc_feature       622..651
FT                      /tag= e
FT                      /note= "Claim 15"
XX
PN   WO9822282-A1.
XX
PD   04-JUN-1998.
XX
PF   26-NOV-1997; 97WO-US021857.
XX
PR   27-NOV-1996; 96US-0031930P.
PR   03-JUN-1997; 97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49041.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
```

PS Claim 9; Fig 16; 47pp; English.
XX
CC This cDNA clone codes for novel human low density lipoprotein (LDL)
CC binding protein LBP-2 (see AAW49041). It was isolated by screening human
CC liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA, cDNA
CC clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
CC 42) are claimed. An abnormality in LBP metabolism or structure is
CC diagnostic of a risk for atherosclerosis. The invention provides: methods
CC for determining if an animal is at risk for atherosclerosis (e.g. for
CC prenatal screening); methods for treating atherosclerosis (including gene
CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC formation of atherosclerotic plaque; and methods for treating a cell
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC vaccine compositions are also provided, as well as recombinant vectors
CC and host cells used to produce recombinant LBP
CC
XX
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:
Score: 0.00852
Percent Similarity: 82.00   Length: 1208
Best Local Similarity: 100.00% Matches: 15
Query Match: 100.00% Conservative: 0
DB: 2   Mismatches: 0
              Indels: 0
              Gaps: 0

US-09-976-740-19 (1-15) x AAV32838 (1-1208)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
   |||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAGATGATGATGATGAAGATGAAGATGAAGAAGATGAT 66

RESULT 4
AAH26494
ID AAH26494 standard; cDNA, 1208 BP.
XX
AC AAH26494;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..654
FT   /*tag= a
FT   /partial
XX
PN WO20016487A-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-0051784.
PR 14-JUL-2000; 2000US-0061689.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR WPI; 2001-565505/63.
DR P-PSDB; AAB28203.
XX
PT New isolated low density lipoprotein binding polypeptide for treating,
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS Example 4; Fig 16; 143pp; English.

XX
CC The present sequence is that of a partial cDNA encoding novel human low
CC density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC isolated from human foetal brain, liver and aorta cDNA libraries using
CC rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC acids are among claimed polynucleotides of the invention that encode
CC novel polypeptides capable of binding to native and methylated LDL. Also
CC claimed are isolated LBP polypeptides, and biologically active fragments
CC and analogues of them, as well as expression vectors, cells and methods
CC of producing the LBPs. Methods of determining if an animal is at risk for
CC atherosclerosis, methods for evaluating an agent for use in treating
CC atherosclerosis, and methods for treating a cell having an abnormality in
CC structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions
CC are also claimed
XX
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:
Score: 0.00852
Percent Similarity: 82.00   Length: 1208
Best Local Similarity: 100.00% Matches: 15
Query Match: 100.00% Conservative: 0
DB: 5   Mismatches: 0
              Indels: 0
              Gaps: 0

US-09-976-740-19 (1-15) x AAH26494 (1-1208)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
   |||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAGATGATGATGATGAAGATGAAGATGAAGAAGATGAT 66

RESULT 5
AAF21860
ID AAF21860 standard; DNA, 1336 BP.
XX
AC AAF21860;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005881.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/58.
DR P-PSDB; AAB58957.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention, treatment
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT neurological diseases.

```
XX
PS   Claim 1; Page 670-671; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC   neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC   antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC   protein sequences are used in the diagnosis of cancer, particularly
CC   breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC   and agonists may also be used in the diagnosis, prevention and treatment
CC   of immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC   cardiovascular disorders such as myocardial ischaemias; wound healing;
CC   neurological diseases such as cerebral anoxia and epilepsy; and
CC   infectious diseases
XX
SQ   Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;

RESULT 6
ID   AAH26499 standard; DNA; 1614 BP.
XX
AC   AAH26499;
XX
DT   12-NOV-2001   (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX

Alignment Scores:
Pred. No.:
Score:                     0.00938
Percent Similarity:        82.00          Length:        1336
Best Local Similarity:    100.00%         Matches:         15
Query Match:              100.00%         Conservative:     0
DB:                          3            Mismatches:       0
                                          Indels:           0
                                          Gaps:             0

US-09-976-740-19 (1-15) x AAF21860 (1-1336)

Qy     1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||||||||
Db    94 GAAGAGGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 138
```

```
XX
PS   Claim 7; Fig 7A; 143pp; English.
XX
CC   The present sequence is that of the coding region of the human gene (see
CC   also AAH26494) encoding novel human low density lipoprotein binding
CC   protein 2 (LBP-2, see AAB28206). The gene was isolated from a genomic DNA
CC   library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the
CC   present sequence differs from that predicted from a cDNA clone (see
CC   AAB82803) in that it contains an additional 321 amino acids at its N-
CC   terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among
CC   claimed polynucleotides of the invention that encode novel polypeptides
CC   capable of binding to native and methylated LDL. Also claimed are
CC   isolated LBP polynucleotides, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Methods of determining if an animal is at risk for
CC   atherosclerosis, methods for evaluating an agent for use in treating
CC   atherosclerosis, and methods for treating a cell having an abnormality in
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;

RESULT 7
ID   AAH26495 standard; DNA; 12425 BP.
XX
AC   AAH26495;
XX
DT   12-NOV-2001   (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) gene.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              2832..5153
FT                    /*tag= a
FT   exon             2832..3785
FT                    /*tag= b
FT                    /note= "includes introns"
FT   intron           3786..4207
FT                    /*tag= c
FT   exon             4208..4502
FT                    /*tag= d
FT   intron           4503..4593
FT                    /*tag= e
FT   exon             4594..4694
FT                    /*tag= f
FT   intron           4695..4787
FT                    /*tag= g
FT   exon             4788..4899
FT                    /*tag= h
FT   intron           4900..4994
FT                    /*tag= i

Alignment Scores:
Pred. No.:
Score:                     0.0112
Percent Similarity:        82.00          Length:        1614
Best Local Similarity:    100.00%         Matches:         15
Query Match:              100.00%         Conservative:     0
DB:                          5            Mismatches:       0
                                          Indels:           0
                                          Gaps:             0

US-09-976-740-19 (1-15) x AAH26499 (1-1614)

Qy     1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||||||||
Db   985 GAAGAGGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 1029
```

```
PN   WO20016487 4-A2.
PD   07-SEP-2001.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
PR   02-MAR-2000; 2000US-0051784 9.
PR   14-JUL-2000; 2000US-006162 89.
PR   28-FEB-2001; 2001WO-US006356.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
```

FT   exon   4995..5153
FT   /*tag= j
XX
PN   WO20016487A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784P.
PR   14-JUL-2000; 2000US-0061628P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 4; Fig 23; 143bp; English.
XX
CC   The present sequence is that of genomic DNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was
CC   isolated from a human genomic library by screening with LBP-2 cDNA (see
CC   AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides, termed LBPs, capable of binding to native and
CC   methylated LDL. Also claimed are isolated LBP polypeptides; and
CC   biologically active fragments and analogues of them, as well as
CC   expression vectors, cells and methods of producing the LBPs. Methods of
CC   determining if an animal is at risk for atherosclerosis, methods for
CC   evaluating an agent for use in treating atherosclerosis, and methods for
CC   treating a cell having an abnormality in structure or metabolism of LBP
CC   are claimed. Pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions, are also claimed.
XX
SQ   Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1
Score: 0.0788   Length: 12425
Percent Similarity: 82.00   Matches: 12425
Best Local Similarity: 100.00%   Conservative: 15
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                          Gaps: 0

US-09-976-740-19 (1-15) x AAH26495 (1-12425)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAspAsp 15
        |||||||||||||||
Db 4238 GAAGAGGAAGAAGAAGATGATGAAGATGAAGATGAAGAAGAAGATGAT 4282

US-09-976-740-19 (1-15)

RESULT 8
AAA70216/c
ID   AAA70216 standard; DNA; 2919 BP.
XX
AC   AAA70216;
XX
DT   07-NOV-2000 (first entry)
XX
DE   Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:349.
KW   Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
KW   antimalarial; malaria; protozoacide; infection; insecticide; ds.
OS   Plasmodium falciparum.
XX
PN   WO20002572B-A2.
XX
PD   11-MAY-2000.

PF   05-NOV-1999; 99WO-US026796.
PR   05-NOV-1998; 98US-0107131P.
XX
PA   (HOFF/) HOFFMAN S.
PA   (CARU/) CARUCCI D.
PA   (GARD/) GARDNER M.
PA   (VENT/) VENTER J C.
XX
PI   Hoffman S, Carucci D, Gardner M, Venter JC;
XX
WPI; 2000-365347/31.
XX
PT   Proteins encoded by chromosome 2 of the human malarial parasite,
PT   Plasmodium falciparum, useful as antimalarial vaccines and in the
PT   diagnosis of P.falciparum infection.
XX
PS   Disclosure; Page 539-540; 577pp; English.
XX
CC   The present invention describes proteins and their fragments (I) encoded
CC   by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
CC   Also described are: (1) nucleotide sequences (II) encoding (I); and (2)
CC   vaccines against P. falciparum infection comprising (I) or (II). (I) and
CC   (II) are useful for the development of vaccines against P. falciparum
CC   infection. (I) and polyclonal antisera or a monoclonal antibody raised to
CC   immunogens comprising the sequences of (I), are useful in the detection
CC   of infection with P. falciparum. Furthermore, (I) (especially when they
CC   are rifins or secreted or membrane proteins) can aid the identification
CC   of drugs to treat or prevent P. falciparum infection, or they can be used
CC   to identify drug resistance in P. falciparum. Sequencing of the
CC   Plasmodium chromosome 2 and the subsequent identification of proteins
CC   encoded by it will help to expand our understanding of parasite biology,
CC   a process hampered by the complexity of the parasitic lifecycle, and
CC   provide new targets for vaccine and drug development. Parasite resistance
CC   to drugs and mosquito resistance to insecticides have led to a resurgence
CC   of malaria in many parts of the world, and there is a pressing need for
CC   vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352
CC   represent nucleotide and protein sequences given in the present
CC   invention, but which are not specifically mentioned within the
CC   specification
XX
SQ   Sequence 2919 BP; 1313 A; 354 C; 392 G; 860 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1
Score: 0.24   Length: 2919
Percent Similarity: 74.00   Matches: 2919
Best Local Similarity: 100.00%   Conservative: 13
Query Match: 86.67%   Mismatches: 2
DB: Indels: 0
                                          Gaps: 0

US-09-976-740-19 (1-15) x AAA70216 (1-2919)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAspAsp 15
        ||||||| ||::|| |||::||
Db 1826 GAAGAAAAGGAAGAACGATGATGAAGATGAAGACGAGGAGGAGGATGAG 1782

RESULT 9
AAZ43754
ID   AAZ43754 standard; cDNA; 2044 BP.
XX
AC   AAZ43754;
XX
DT   24-FEB-2000 (first entry)
XX
DE   Murine NNX3 cDNA.
KW   NNX3; murine; cytostatic; marker; lung tumor; Hodgkin's disease;
KW   treatment; ds.
OS   Mus musculus.
XX

Left column

```
FH    Key              Location/Qualifiers
FT    CDS              77..1450
FT                     /*tag= a
FT                     /product= "NNX3"
XX
PN    WO9960115-A2.
XX
PD    25-NOV-1999.
XX
PF    17-MAY-1999;      99WO-EP003374.
XX
PR    18-MAY-1998;      98EP-00201642.
XX
PA    (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI    Van Leuven F;
XX
DR    WPI; 2000-053295/04.
DR    P-PSDB; AAY50875.
XX
PT    Novel proteins useful as markers and for treating lung tumors and/or
PT    Hodgkin's disease.
XX
PS    Claim 5; Page 45-47; 50pp; English.
XX
CC    This invention describes two novel NNX3 proteins isolated from human and
CC    murine sources which have cytostatic activity. The NNX3 mRNA and/or
CC    protein is useful as a marker for lung tumors or Hodgkin's disease. The
CC    proteins form pharmaceutical compositions useful for treating lung tumors
CC    and/or Hodgkin's disease. Polynucleotide products of the invention form
CC    an assay for screening the expression of these nucleic acids. Antibodies
CC    raised against the proteins of the invention form an assay for detecting
CC    the proteins. The probes form an assay for detecting and/or amplifying
CC    NNX3 polynucleotides. The expression of NNX3 in humans and mice suggest
CC    that NNX3 is useful as a marker for lung tumors and Hodgkin's disease.
CC    Therefore, the protein facilitates therapies for these conditions. This
CC    sequence encodes the murine NNX3 protein described in the method of the
CC    invention
XX
SQ    Sequence 2044 BP; 630 A; 400 C; 482 G; 532 T; 0 U; 0 Other;
XX
XX

Qy    US-09-976-740-19 (1-15) x AAZ43754 (1-2044)

Alignment Scores:
Pred. No.:
Score:                 0.234
                       73.00
Percent Similarity:    100.00%        Length:        2044
Best Local Similarity: 80.00%         Matches:       12
Query Match:           89.02%         Conservative:  3
                                      Mismatches:    0
                                      Indels:        0
                                      Gaps:          0

Qy     1 GluGluGluGluAspAspAspGluAspGluAspGluGluGluAsp 15
         |||||||||||||:::|||||||:|||||||||||||||||||
Db    761 GAAGAAGAAGAAGATGACGATGATGATGATGATGAAGATGACGAT 805
```

```
RESULT 10
      AAT27052
ID    AAT27052 standard; DNA; 4599 BP.
AC    AAT27052;
XX
DT    12-OCT-1996  (first entry)
XX
DE    RRP3 telomerase-associated protein gene.
XX
KW    Yeast; RRP3 gene; telomerase-associated protein; STR7;
KW    suppressor of telomeric repression-7; telomerase; ribonucleoprotein;
KW    telomere; tumour; pathogen; sperm; ovum; reporter gene; drug screening;
KW    antibody; immunoassay; antitumour; antiseptic; contraceptive;
KW    infertility; diagnostic; gene therapy; ss.
XX
OS    Saccharomyces cerevisiae.
XX
```

Right column

```
FH    Key              Location/Qualifiers
FT    CDS              835..4092
FT                     /*tag= a
FT                     /product= "RRP3 protein"
XX
PN    WO9612811-A2.
XX
PD    02-MAY-1996.
XX
PF    20-OCT-1995;      95WO-US013801.
XX
PR    20-OCT-1994;      94US-00326781.
PR    28-APR-1995;      95US-00431080.
XX
PA    (ARCH-) ARCH DEV CORP.
XX
PI    Gottschling DE,  Singer MS;
XX
DR    WPI; 1996-239169/24.
DR    P-PSDB; AAR95607.
XX
PT    Novel telomerase associated polypeptide(s) and related nucleic acid -
PT    useful for detecting e.g. tumour cells or pathogens.
XX
PS    Example 10; Page 287-293; 349pp; English.
XX
CC    The RRP3 gene encodes a telomerase-associated protein (with a fragment,
CC    STR7, shown in AAT27051) found in conjunction with Saccharomyces
CC    cerevisiae telomerase, a ribonucleoprotein required for telomere
CC    replication. Other genes associated with telomerase are given in AAT27045
CC    (telomerase RNA template gene) and AAT27046-50 (other STR genes). These
CC    genes combine with telomerase to repress telomere silencing of gene
CC    expression. Oligonucleotides from the sequence may be used to detect non-
CC    ciliate telomerase-associated genes, e.g. in tumour, pathogen, sperm or
CC    ovum cells. New telomerase-associated sequences may be detected by a
CC    reporter gene expression system linked to an expression-repressing
CC    telomere sequence, and binding compounds, e.g. antibodies, may be
CC    detected by complex formation with telomerase components. The products
CC    may be used as antitumour, antiseptic or contraceptive agents, in
CC    infertility diagnosis, or in gene therapy
XX
SQ    Sequence 4599 BP; 1717 A; 779 C; 898 G; 1205 T; 0 U; 0 Other;
XX
XX

Qy    US-09-976-740-19 (1-15) x AAT27052 (1-4599)

Alignment Scores:
Pred. No.:
Score:                 0.506
                       73.00
Percent Similarity:    100.00%         Length:        4599
Best Local Similarity: 80.00%          Matches:       12
Query Match:           89.02%          Conservative:  3
                                       Mismatches:    0
                                       Indels:        0
                                       Gaps:          0

Qy      1 GluGluGluGluAspAspAspGluAspGluAspGluGluGluAsp 15
          ||||||||||||:::||||||||:||||||||||||||||||||
Db    1231 GAAGAAGAAGAAGATGACGATGACGAAGACGAAGACGACGATGATGAT 1275
```

```
RESULT 11
      AAC44095
ID    AAC44095 standard; DNA; 643 BP.
AC    AAC44095;
XX
DT    18-OCT-2000  (first entry)
XX
DE    Arabidopsis thaliana DNA fragment SEQ ID NO: 41614.
XX
KW    Hybridisation assay; genetic mapping; gene expression control;
KW    protein identification; signal transduction pathway; metabolic pathway;
KW    promoter; termination sequence; ss.
XX
OS    Arabidopsis thaliana.
XX
```

```
PN   EP103340S-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-00301439.
XX
PR   25-FEB-1999; 99US-0121825P.
PR   05-MAR-1999; 99US-0123180P.
PR   09-MAR-1999; 99US-0123548P.
PR   23-MAR-1999; 99US-0125788P.
PR   25-MAR-1999; 99US-0126264P.
PR   29-MAR-1999; 99US-0126785P.
PR   01-APR-1999; 99US-0127462P.
PR   06-APR-1999; 99US-0128234P.
PR   08-APR-1999; 99US-0128714P.
PR   16-APR-1999; 99US-0129845P.
PR   19-APR-1999; 99US-0130077P.
PR   21-APR-1999; 99US-0130449P.
PR   23-APR-1999; 99US-0130510P.
PR   28-APR-1999; 99US-0130891P.
PR   30-APR-1999; 99US-0131449P.
PR   30-APR-1999; 99US-0132048P.
PR   04-MAY-1999; 99US-0132407P.
PR   05-MAY-1999; 99US-0132484P.
PR   06-MAY-1999; 99US-0132485P.
PR   06-MAY-1999; 99US-0132486P.
PR   07-MAY-1999; 99US-0132863P.
PR   11-MAY-1999; 99US-0134256P.
PR   14-MAY-1999; 99US-0134218P.
PR   14-MAY-1999; 99US-0134219P.
PR   14-MAY-1999; 99US-0134221P.
PR   13-MAY-1999; 99US-0134370P.
PR   18-MAY-1999; 99US-0134768P.
PR   19-MAY-1999; 99US-0134941P.
PR   20-MAY-1999; 99US-0135124P.
PR   21-MAY-1999; 99US-0135353P.
PR   24-MAY-1999; 99US-0135629P.
PR   25-MAY-1999; 99US-0136021P.
PR   27-MAY-1999; 99US-0136392P.
PR   28-MAY-1999; 99US-0136782P.
PR   01-JUN-1999; 99US-0137222P.
PR   03-JUN-1999; 99US-0137528P.
PR   04-JUN-1999; 99US-0137502P.
PR   07-JUN-1999; 99US-0137724P.
PR   08-JUN-1999; 99US-0138094P.
PR   10-JUN-1999; 99US-0138540P.
PR   14-JUN-1999; 99US-0138847P.
PR   16-JUN-1999; 99US-0139119P.
PR   16-JUN-1999; 99US-0139452P.
PR   17-JUN-1999; 99US-0139453P.
PR   18-JUN-1999; 99US-0139456P.
PR   18-JUN-1999; 99US-0139457P.
PR   18-JUN-1999; 99US-0139458P.
PR   18-JUN-1999; 99US-0139459P.
PR   18-JUN-1999; 99US-0139460P.
PR   18-JUN-1999; 99US-0139461P.
PR   18-JUN-1999; 99US-0139462P.
PR   18-JUN-1999; 99US-0139463P.
PR   18-JUN-1999; 99US-0139750P.
PR   18-JUN-1999; 99US-0139763P.
PR   21-JUN-1999; 99US-0139817P.
PR   22-JUN-1999; 99US-0139999P.
PR   23-JUN-1999; 99US-0140333P.
PR   23-JUN-1999; 99US-0140354P.
PR   24-JUN-1999; 99US-0140695P.
PR   28-JUN-1999; 99US-0140823P.
PR   29-JUN-1999; 99US-0140991P.
PR   30-JUN-1999; 99US-0141287P.
PR   01-JUL-1999; 99US-0141842P.

PR   01-JUL-1999; 99US-0142154P.
PR   02-JUL-1999; 99US-0142055P.
PR   06-JUL-1999; 99US-0142390P.
PR   08-JUL-1999; 99US-0142803P.
PR   09-JUL-1999; 99US-0142920P.
PR   12-JUL-1999; 99US-0142977P.
PR   13-JUL-1999; 99US-0143542P.
PR   14-JUL-1999; 99US-0143624P.
PR   15-JUL-1999; 99US-0144005P.
PR   16-JUL-1999; 99US-0144086P.
PR   16-JUL-1999; 99US-0144325P.
PR   19-JUL-1999; 99US-0144331P.
PR   19-JUL-1999; 99US-0144332P.
PR   19-JUL-1999; 99US-0144333P.
PR   19-JUL-1999; 99US-0144335P.
PR   20-JUL-1999; 99US-0144352P.
PR   20-JUL-1999; 99US-0144632P.
PR   20-JUL-1999; 99US-0144884P.
PR   21-JUL-1999; 99US-0144814P.
PR   21-JUL-1999; 99US-0450862P.
PR   22-JUL-1999; 99US-0450882P.
PR   22-JUL-1999; 99US-0451192P.
PR   23-JUL-1999; 99US-0451145P.
PR   23-JUL-1999; 99US-0452187P.
PR   23-JUL-1999; 99US-0452247P.
PR   26-JUL-1999; 99US-0452765P.
PR   27-JUL-1999; 99US-0459137P.
PR   27-JUL-1999; 99US-0459187P.
PR   27-JUL-1999; 99US-0459197P.
PR   28-JUL-1999; 99US-0459512P.
PR   02-AUG-1999; 99US-0463862P.
PR   02-AUG-1999; 99US-0463888P.
PR   02-AUG-1999; 99US-0463889P.
PR   03-AUG-1999; 99US-0470382P.
PR   04-AUG-1999; 99US-0470382P.
PR   04-AUG-1999; 99US-0472204P.
PR   05-AUG-1999; 99US-0471192P.
PR   05-AUG-1999; 99US-0472260P.
PR   06-AUG-1999; 99US-0472303P.
PR   06-AUG-1999; 99US-0474416P.
PR   09-AUG-1999; 99US-0474493P.
PR   09-AUG-1999; 99US-0477935P.
PR   10-AUG-1999; 99US-0481171P.
PR   11-AUG-1999; 99US-0483319P.
PR   12-AUG-1999; 99US-0483341P.
PR   13-AUG-1999; 99US-0486684P.
PR   13-AUG-1999; 99US-0488565P.
PR   17-AUG-1999; 99US-0491175P.
PR   18-AUG-1999; 99US-0494426P.
PR   20-AUG-1999; 99US-0497223P.
PR   20-AUG-1999; 99US-0497233P.
PR   20-AUG-1999; 99US-0497292P.
PR   23-AUG-1999; 99US-0499299P.
PR   23-AUG-1999; 99US-0499902P.
PR   25-AUG-1999; 99US-0499302P.
PR   26-AUG-1999; 99US-0150566P.
PR   27-AUG-1999; 99US-0150884P.
PR   27-AUG-1999; 99US-0151065P.
PR   27-AUG-1999; 99US-0151066P.
PR   30-AUG-1999; 99US-0151080P.
PR   31-AUG-1999; 99US-0151303P.
PR   01-SEP-1999; 99US-0151438P.
PR   07-SEP-1999; 99US-0151930P.
PR   10-SEP-1999; 99US-0152363P.
PR   13-SEP-1999; 99US-0153070P.
PR   15-SEP-1999; 99US-0153758P.
PR   16-SEP-1999; 99US-0154018P.
PR   16-SEP-1999; 99US-0154039P.
```

PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0192924P.
PR 13-OCT-1999; 99US-0192925P.
PR 14-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159377P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 28-OCT-1999; 99US-0160768P.
PR 28-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 29-OCT-1999; 99US-0161993P.
PR 28-OCT-1999; 99US-0161992P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.:
Score: 0.106
Percent Similarity: 72.00
                     100.00%
Best Local Similarity: 80.00%
Query Match: 87.80%
DB:

US-09-976-740-19 (1-15) x AAC44095 (1-643)

Length: 643
Matches: 12
Conservative: 3
Mismatches: 0
Indels: 0
Gaps: 0

Qy   1 GluGluGluLuAspAspGluAspGluGluAspAsp 15
          |||||||||||||||::|||||||||||||::|||
Db   596 GAAGAGGAAGAAGATGACGATGATGAATGACGACGAGGAGGAAGAAGAC 640

RESULT 12
ABN98791
ID   ABN98791 standard; DNA; 872 BP.
XX
AC   ABN98791;
XX
DT   01-AUG-2002 (first entry)
XX
DE   Arabidopsis thaliana expressed polynucleotide SEQ ID NO 559.
XX
KW   Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
KW   disease; crop; thale cress; tolerance factor; insect; pathogen;
KW   nutrition; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   US20020023281-A1.

PS   Claim 1; SEQ ID NO 559; 49pp + Sequence Listing; English.
XX
XX
CC   New Arabidopsis thaliana nucleic acid for identifying homologous genes,
CC   producing compositions that modulate the expression or function of its
CC   encoded protein, and mapping functional regions of protein.
XX
CC   The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC   comprising a sequence capable of hybridising under stringent conditions
CC   to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC   given in the specification or its fragment. A polypeptide (III) encoded by
CC   (I), a transgenic plant (III) comprising an exogenous nucleic acid, or a
CC   genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC   useful for screening a candidate agent for its biological effect. (I) is
CC   useful in identifying homologous or related genes in producing
CC   compositions that modulate the expression or function of its encoded
CC   protein, mapping functional regions of the protein and in studying
CC   associated physiological pathways. (I) is also useful for the genetic
CC   manipulation of cells, particularly plant cells. (I) is also useful in
CC   screening assays of various plant strains to determine the strains that
CC   are best capable of withstanding a particular disease or environmental
CC   stress. (II) and (III) are useful for screening of biologically active
CC   agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC   pathways. The screened agents are useful in improved methods of treating
CC   crops to prevent or treat disease. (II) are also useful in screening
CC   programs to identify agents that mimic or enhance the action of tolerance
CC   factors. Such agents are useful in improved methods of treating crops to
CC   enhance their tolerance to environmental stress. (I) is also useful for
CC   enhancing or inhibiting production of a biosynthetic product in a plant.
CC   (III) is useful for identifying other mediators that may induce
CC   expression of proteins of interest, for establishing the extent to which
CC   any specific insect and/or pathogen is responsible for damage to a
CC   particular plant, for identifying other mediators that enhance or induce
CC   tolerance to environmental stress, for identifying factors involved in
CC   biosynthetic pathways of nutritional, commercial, or medicinal value and
CC   for identifying productions of nutritional, commercial or medicinal
CC   value. (IV) is useful in the study of genetic function and regulation,
CC   for alteration of the cellular metabolism and for screening compounds
CC   that may affect the biological function of the gene or gene products.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO

```
CC    at seqdata.uspto.gov/sequence.html?DocID=999090770445
XX
SQ    Sequence 872 BP; 326 A; 132 C; 208 G; 193 T; 0 U; 13 Other;

Alignment Scores:

Pred. No.:                  0.142
Score:                     72.00
Percent Similarity:       100.00%
Best Local Similarity:     80.00%
Query Match:               87.80%

                  Length:        872      Matches:       12
                  Conservative:    3      Mismatches:     0
                  Indels:          0      Gaps:           0
DB:

US-09-976-740-19 (1-15) x A8N98791 (1-872)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluGluAspGluGluAspAsp  15
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 GAAGAGGAAGAGAAGAGGATGACGATGATGATGACCAGACGAGGAAGAAGAC 577

RESULT 13
AAC42206
ID    AAC42206 standard; DNA; 893 BP.
XX
AC    AAC42206;
XX
DT    17-OCT-2000 (first entry)
XX
DE    Arabidopsis thaliana DNA fragment SEQ ID NO: 34680.
XX
KW    Hybridisation assay; genetic mapping; gene expression control;
KW    protein identification; signal transduction pathway; metabolic pathway;
KW    promoter; termination sequence; ss.
XX
OS    Arabidopsis thaliana.
XX
PN    EP1033405-A2.
XX
PD    06-SEP-2000.
XX
PF    25-FEB-2000; 2000EP-0301439.
```

PR   25-FEB-1999; 99US-0121825P.
PR   05-MAR-1999; 99US-0123180P.
PR   09-MAR-1999; 99US-0123548P.
PR   23-MAR-1999; 99US-0125788P.
PR   25-MAR-1999; 99US-0126264P.
PR   29-MAR-1999; 99US-0126785P.
PR   01-APR-1999; 99US-0127462P.
PR   06-APR-1999; 99US-0128234P.
PR   08-APR-1999; 99US-0128714P.
PR   16-APR-1999; 99US-0129845P.
PR   19-APR-1999; 99US-0130077P.
PR   21-APR-1999; 99US-0130449P.
PR   23-APR-1999; 99US-0130510P.
PR   28-APR-1999; 99US-0131449P.
PR   30-APR-1999; 99US-0132048P.
PR   04-MAY-1999; 99US-0132407P.
PR   05-MAY-1999; 99US-0132484P.
PR   06-MAY-1999; 99US-0132485P.
PR   06-MAY-1999; 99US-0132486P.
PR   07-MAY-1999; 99US-0132663P.
PR   11-MAY-1999; 99US-0132556P.
PR   14-MAY-1999; 99US-0134218P.
PR   14-MAY-1999; 99US-0134219P.
PR   14-MAY-1999; 99US-0134221P.
PR   14-MAY-1999; 99US-0134770P.
PR   18-MAY-1999; 99US-0134768P.
PR   19-MAY-1999; 99US-0134941P.
PR   20-MAY-1999; 99US-0135124P.
PR   21-MAY-1999; 99US-0135353P.
PR   24-MAY-1999; 99US-0135629P.
PR   25-MAY-1999; 99US-0136021P.

PR   27-MAY-1999; 99US-0136392P.
PR   28-MAY-1999; 99US-0136782P.
PR   01-JUN-1999; 99US-0137222P.
PR   03-JUN-1999; 99US-0137528P.
PR   04-JUN-1999; 99US-0137502P.
PR   07-JUN-1999; 99US-0137724P.
PR   08-JUN-1999; 99US-0138094P.
PR   10-JUN-1999; 99US-0138540P.
PR   10-JUN-1999; 99US-0138447P.
PR   14-JUN-1999; 99US-0139119P.
PR   16-JUN-1999; 99US-0139452P.
PR   17-JUN-1999; 99US-0139492P.
PR   18-JUN-1999; 99US-0139454P.
PR   18-JUN-1999; 99US-0139455P.
PR   18-JUN-1999; 99US-0139456P.
PR   18-JUN-1999; 99US-0139462P.
PR   18-JUN-1999; 99US-0139463P.
PR   18-JUN-1999; 99US-0139458P.
PR   18-JUN-1999; 99US-0139459P.
PR   18-JUN-1999; 99US-0139460P.
PR   18-JUN-1999; 99US-0139461P.
PR   18-JUN-1999; 99US-0139750P.
PR   18-JUN-1999; 99US-0139763P.
PR   21-JUN-1999; 99US-0139817P.
PR   22-JUN-1999; 99US-0139899P.
PR   23-JUN-1999; 99US-0140353P.
PR   23-JUN-1999; 99US-0140325P.
PR   24-JUN-1999; 99US-0140695P.
PR   28-JUN-1999; 99US-0140823P.
PR   29-JUN-1999; 99US-0140991P.
PR   30-JUN-1999; 99US-0141287P.
PR   01-JUL-1999; 99US-0141842P.
PR   01-JUL-1999; 99US-0141842P.
PR   02-JUL-1999; 99US-0121542P.
PR   06-JUL-1999; 99US-0142055P.
PR   06-JUL-1999; 99US-0142390P.
PR   08-JUL-1999; 99US-0142803P.
PR   09-JUL-1999; 99US-0142920P.
PR   12-JUL-1999; 99US-0142977P.
PR   13-JUL-1999; 99US-0143542P.
PR   14-JUL-1999; 99US-0143624P.
PR   15-JUL-1999; 99US-0144005P.
PR   16-JUL-1999; 99US-0144085P.
PR   16-JUL-1999; 99US-0144086P.
PR   19-JUL-1999; 99US-0144325P.
PR   19-JUL-1999; 99US-0144331P.
PR   19-JUL-1999; 99US-0144332P.
PR   19-JUL-1999; 99US-0144333P.
PR   19-JUL-1999; 99US-0144334P.
PR   19-JUL-1999; 99US-0144335P.
PR   20-JUL-1999; 99US-0144632P.
PR   20-JUL-1999; 99US-0144884P.
PR   21-JUL-1999; 99US-0144814P.
PR   21-JUL-1999; 99US-0145086P.
PR   21-JUL-1999; 99US-0145088P.
PR   22-JUL-1999; 99US-0145089P.
PR   22-JUL-1999; 99US-0145087P.
PR   22-JUL-1999; 99US-0145192P.
PR   23-JUL-1999; 99US-0145145P.
PR   23-JUL-1999; 99US-0145218P.
PR   23-JUL-1999; 99US-0145224P.
PR   26-JUL-1999; 99US-0145276P.
PR   27-JUL-1999; 99US-0145913P.
PR   27-JUL-1999; 99US-0145918P.
PR   27-JUL-1999; 99US-0145919P.
PR   28-JUL-1999; 99US-0145951P.
PR   02-AUG-1999; 99US-0146763P.
PR   02-AUG-1999; 99US-0146866P.
PR   02-AUG-1999; 99US-0146388P.
PR   03-AUG-1999; 99US-0147038P.

PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147915P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149720P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156560P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159377P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 25-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161993P.
PR 28-OCT-1999; 99US-0161993P.

PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.:   0.145
Score: 72.00
Percent Similarity: 100.00%
Best Local Similarity: 80.00%
Query Match: 87.80%
DB:

Length: 893
Matches: 12
Conservative: 3
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x AAC42206 (1-893)

Qy 1 GluGluGluAspAspAspGluAspGluGluAspAsp 15
        |||||||||||||||||||:|||||||||:|||||||
Db 596 GAAGAGGAAGAAGATGACGATGATGACGACGAGGAGGAAGAGAC 640

RESULT 14
AB232099
ID AB232099 standard; DNA; 1284 BP.
XX
AC AB232099;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans essential gene SEQ ID NO 6386.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; gene; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-02259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
DR P-PSDB; ABP73549.
XX
PT Claim 37; SEQ ID NO 6386; 167pp + Sequence Listing; English.
XX
PS
CC
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division

CC   activity. The method is useful for identifying a compound having the
CC   ability to inhibit growth or proliferation of C. albicans cells and for
CC   treating infection by C. albicans. The present sequence is that of an
CC   essential Candida albicans gene used in the method of the invention.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification but is based on sequence information supplied to Derwent by
CC   the European Patent Office
XX
SQ   Sequence 1284 BP; 581 A; 156 C; 255 G; 292 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 0.205
Percent Similarity: 72.00
Best Local Similarity: 100.00%
Query Match: 80.00%
DB: 87.80%

Length: 1284
Matches: 12
Conservative: 3
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x ABZ32099 (1-1284)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
        ||||||||||||||||||||||||||||||||||||||||
Db 400 GAGGAGGAAGAGGATCGATGACGACGACGATGAAGAAGAGGATGAC 444

RESULT 15
ABQ76615/c
ID   ABQ76615 standard; cDNA; 15790 BP.
XX
AC   ABQ76615;
XX
DT   21-NOV-2002 (first entry)
XX
DE   C. albicans BAX-associated cDNA fragment SEQ ID 655.
XX
KW   Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW   vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW   apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW   neurodegeneration; cell death; ss.
XX
OS   Candida albicans.
XX
PN   WO200264766-A2.
XX
PD   22-AUG-2002.
XX
PF   21-DEC-2001; 2001WO-EP015398.
XX
PR   22-DEC-2000; 2000EP-00870318.
PR   04-JAN-2001; 2001EP-00870002.
PR   09-JAN-2001; 2001EP-00870003.
XX
PA   (JANC) JANSSEN PHARM NV.
XX
PI   Contreras RH, Eberhardt I, Luyten WHM, Reekmans RJ;
XX
DR   WPI; 2002-667002/71.
DR   P-PSDB; ABG93349.
XX
PT   New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT   medicament for treating, preventing and/or alleviating yeast or fungal
PT   infections or proliferative disorders, or for preventing apoptosis in
PT   certain diseases.
XX
PS   Claim 36; Fig 2; 344pp; English.
XX
CC   This invention describes a novel nucleic acid representing a synthetic
CC   Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC   resistant yeast or fungi, identifying, or obtaining and identifying
CC   Candida spp. sequences that are differentially expressed in a pathway
CC   eventually leading to programmed cell death or identifying inhibitors or
CC   inhibitor sequences of Bax-induced cell death. The products of the
CC   invention have cytostatic, fungicide, immunosuppressive, virucide and
CC   vasotropic activity and can be used in vaccines or for gene therapy. The

CC   isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC   antisense molecules and antibodies are useful as medicaments or in
CC   preparing a medicament for treating, preventing and/or alleviating
CC   diseases associated with yeast or fungi or proliferative disorders, such
CC   as cancer, or for preventing apoptosis in certain diseases. The compounds
CC   or polypeptides, or the genetically modified organism are useful for
CC   preparing a medicament for modifying the endogenic flora of humans and
CC   other mammals. The vaccine is useful for immunising against yeast or
CC   fungal infections. Apoptosis-related diseases include autoimmune disease,
CC   ischaemia, diseases related with viral infections or neurodegenerations.
CC   This sequence represents a polynucleotide associated with the Bax gene
CC   described in the disclosure of the invention
XX
SQ   Sequence 15790 BP; 5181 A; 2570 C; 2199 G; 5840 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 2.25
Percent Similarity: 72.00
Best Local Similarity: 100.00%
Query Match: 80.00%
DB: 87.80%

Length: 15790
Matches: 12
Conservative: 3
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x ABQ76615 (1-15790)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
          ||||||||||||||||||||||||||||||||||||||||
Db 12097 GAGGAGGAAGAGGATGATGACGACGACGATGAAGAAGAGGATGAC 12053

Search completed: March 12, 2004, 21:08:29
Job time : 31.776 secs

OM protein - nucleic search, using frame_plus_p2n model

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

Run on: March 12, 2004, 20:05:17 ; Search time 5.08568 Seconds
(without alignments)
1636.805 Million cell updates/sec

Title: US-09-976-740-19
Perfect score: 82
Sequence: 1 EEEEDDDEDEDEDD 15

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+_p2n.model
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US0997674O/runat 10032004 094549 19564/app_query.fasta_1.1898
-Q=/cgn2_1/USPTO_spool_p/US0997674O/runat 10032004 094549 19564/app_query.fasta_1.1898
-DB=issued Patents.NA. -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0997674O @CGN 1 1 235 @runat 10032004 094549 19564 -NCPU=6 ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	* DB	ID	Description
1	82	100.0	45	4	US-08-979-608A-30	Sequence 30, Appli
2	82	100.0	45	4	US-09-517-849-30	Sequence 30, Appli
3	82	100.0	45	4	US-09-616-289-30	Sequence 30, Appli
4	82	100.0	78	4	US-08-979-608A-31	Sequence 31, Appl
5	82	100.0	78	4	US-09-517-849-31	Sequence 31, Appl
6	82	100.0	78	4	US-09-616-289-31	Sequence 31, Appl
7	82	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appli
8	82	100.0	1208	4	US-09-517-849-16	Sequence 16, Appli
9	82	100.0	1208	4	US-09-616-289-16	Sequence 16, Appli
10	82	100.0	1614	4	US-09-616-289-45	Sequence 45, Appl
11	82	100.0	12425	4	US-09-616-289-50	Sequence 50, Appl
12	73	89.0	4599	1	US-08-431-080-27	Sequence 27, Appl

13	73	89.0	4599	2	US-09-938-534-27	Sequence 27, Appl
14	73	89.0	4599	2	US-09-345-294-27	Sequence 27, Appl
15	72	86.6	2736	4	US-09-220-132-66	Sequence 66, Appl
16	71	86.6	7585	4	US-09-418-710-22	Sequence 22, Appli
17	71	85.4	956	1	US-08-431-080-25	Sequence 25, Appl
18	70	85.4	956	1	US-08-431-080-32	Sequence 32, Appli
19	70	85.4	956	2	US-09-938-534-25	Sequence 25, Appl
20	70	85.4	956	2	US-09-938-534-32	Sequence 32, Appli
21	70	85.4	956	4	US-09-345-294-25	Sequence 25, Appli
22	70	85.4	956	4	US-09-345-294-32	Sequence 32, Appl
23	70	85.4	1194	3	US-09-220-132-31	Sequence 31, Appl
24	70	85.4	2518	3	US-09-433-699-3	Sequence 3, Appli
25	70	85.4	5751	4	US-09-023-655-1415	Sequence 1415, Ap
26	70	85.4	11907	1	US-08-061-376-4	Sequence 4, Appli
27	70	85.4	14255	1	US-08-320-559-1	Sequence 1, Appl
28	70	85.4	14255	1	US-08-327-392-1	Sequence 1, Appli
29	70	85.4	14255	1	US-08-306-691B-55	Sequence 55, Appli
30	70	85.4	14255	3	US-08-545-860D-1	Sequence 1, Appli
31	69	85.4	14255	5	PCT-US94-04496-1	Sequence 1, Appli
32	69	84.1	1275	1	US-08-552-142A-3	Sequence 3, Appli
33	69	84.1	1275	1	US-08-910-973-3	Sequence 3, Appli
34	69	84.1	1275	3	US-09-499-227-3	Sequence 3, Appli
35	69	84.1	1275	5	PCT-US95-05741-3	Sequence 3, Appli
36	69	84.1	2101	2	US-08-568-459A-9	Sequence 9, Appli
37	69	84.1	2101	2	US-08-487-826B-9	Sequence 9, Appli
38	69	84.1	2101	2	US-09-210-288-9	Sequence 9, Appli
39	69	84.1	7295	2	US-08-487-826B-15	Sequence 15, Appl
40	68	82.9	2581	4	US-08-370-838-166	Sequence 166, Appl
41	68	82.9	3164	4	US-09-023-655-816	Sequence 816, App
42	68	82.9	3489	2	US-08-728-323A-1	Sequence 1, Appli
43	68	82.9	3489	4	US-08-298-568-1	Sequence 1, Appli
44	68	82.9	3489	4	US-09-410-999-1	Sequence 1, Appli
45	68	82.9	32207	2	US-08-770-379-20	Sequence 20, Appl

RESULT 1
US-08-979-608A-30

Sequence 30, Application US/08979608A

Patent No. 6355451

; Patent No. 6355451 Application US/08979608A

GENERAL INFORMATION:

APPLICANT:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965

ALIGNMENTS

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..45
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-08-979-608A-30

Alignment Scores:
; Pred. No.:
; Score: 4.28e-05
; Percent Similarity: 82.00
; Best Local Similarity: 100.00%
; Query Match: 100.00%
; DB: 4

Length: 45
Matches: 15
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x US-08-979-608A-30 (1-45)

Qy   1 GluGluGluGluAspAspAspAspGluAspGluGluAspAsp 15
        ||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAGGAAGATGATGATGATGAAGATGAAGAAGATGAT 45

RESULT 2
US-09-517-849-30
; Sequence 30, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; ZIP: 02110-2804
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,849
; FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..45
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-517-849-30

Alignment Scores:
; Pred. No.:
; Score: 4.28e-05
; Percent Similarity: 82.00
; Best Local Similarity: 100.00%
; Query Match: 100.00%
; DB: 4

Length: 45
Matches: 15
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x US-09-517-849-30 (1-45)

Qy   1 GluGluGluGluAspAspAspAspGluAspGluGluAspAsp 15
        ||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAGGAAGATGATGATGATGAAGATGAAGAAGATGAT 45

RESULT 3
US-09-616-289-30
; Sequence 30, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-616-289-30

Alignment Scores:
; Pred. No.:
; Score: 4.28e-05
; Percent Similarity: 82.00
; Best Local Similarity: 100.00%
; Query Match: 100.00%
; DB: 4

Length: 45
Matches: 15
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-30 (1-45)

Qy   1 GluGluGluGluAspAspAspAspGluAspGluGluAspAsp 15
        ||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAGGAAGATGATGATGATGAAGATGAAGAAGATGAT 45

RESULT 4
US-08-979-608A-31
; Sequence 31, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
   TREATING ATHEROSCLEROSIS
   Law, Simon W.
   Arjona, Anibal A.
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Fish & Richardson P.C.
   STREET: 225 Franklin Street
   CITY: Boston
   STATE: MA
   COUNTRY: USA
   ZIP: 02110-2804
COMPUTER READABLE FORM:
   MEDIUM TYPE: Diskette
   COMPUTER: IBM Compatible
   OPERATING SYSTEM: DOS
   SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/979,608A
   FILING DATE: 26-NO. 635451-1997
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 60/048,547
   FILING DATE: 03-JUN-1997
   APPLICATION NUMBER: US 60/031,930
   FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
   NAME: Myers, Louis
   REGISTRATION NUMBER: 35,965
   REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 617/542-5070
   TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 78 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   FEATURE:
   NAME/KEY: Coding Sequence
   LOCATION: 1..78
   SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-08-979-608A-31

Alignment Scores:
   Pred. No.:   7.31e-05
   Score: 82.00
   Percent Similarity: 100.00%   Length: 78
   Best Local Similarity: 100.00%   Matches: 15
   Query Match: 100.00%   Conservative: 0
   DB: 4   Mismatches: 0
                                          Indels: 0
                                          Gaps: 0

US-09-976-740-19 (1-15) x US-08-979-608A-31 (1-78)
Qy 1 GluGluGluLuAspPAspPAspGluAspGluAspGluGluAspPAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAAGATGAT 45

RESULT 5
US-09-517-849-31
Sequence 31, Application US/0951784 9
Patent No. 6605588
GENERAL INFORMATION:
   APPLICANT: Lees, Ann M.
       Lees, Robert S.
       Law, Simon W.
       Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
   TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

   ADDRESSEE: Fish & Richardson P.C.
   STREET: 225 Franklin Street
   CITY: Boston
   STATE: MA
   COUNTRY: USA
   ZIP: 02110-2804
COMPUTER READABLE FORM:
   MEDIUM TYPE: Diskette
   COMPUTER: IBM Compatible
   OPERATING SYSTEM: DOS
   SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/517,849
   FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 08/979,608
   FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
   NAME: Myers, Louis
   REGISTRATION NUMBER: 35,965
   REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 617/542-5070
   TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 78 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   FEATURE:
   NAME/KEY: Coding Sequence
   LOCATION: 1..78
   SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-517-849-31

Alignment Scores:
   Pred. No.:   7.31e-05
   Score: 82.00
   Percent Similarity: 100.00%   Length: 78
   Best Local Similarity: 100.00%   Matches: 15
   Query Match: 100.00%   Conservative: 0
   DB: 4   Mismatches: 0
                                          Indels: 0
                                          Gaps: 0

US-09-976-740-19 (1-15) x US-09-517-849-31 (1-78)
Qy 1 GluGluGluLuAspPAspPAspGluAspGluAspGluGluAspPAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAAGATGAT 45

RESULT 6
US-09-616-289-31
Sequence 31, Application US/0961628 9
Patent No. 6632923
GENERAL INFORMATION:
   APPLICANT: Lees, Ann M.
   APPLICANT: Lees, Robert S.
   APPLICANT: Law, Simon W.
   APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
   PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
   ATHEROSCLEROSIS
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
   PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
   ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
FILE REFERENCE: 10797-004001
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03

```
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-616-289-31
```

Alignment Scores:
Pred. No.:
Score: Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-31 (1-78)

```
Qy    1 GluGluGluLuAspAspAspGluAspGluLuAspGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAGAGGAAGAAGAATGATGATGATGAAGATGAAGATGAAGAAGATGAT 45
```

RESULT 7
US-08-979-608A-16
; Sequence 16, Application US/0897960BA
; Patent No. 6355451
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
             Lees, Robert S.
             Law, Simon W.
             Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
       TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/979,608A
    FILING DATE: 26-No. 6355451-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/048,547
    FILING DATE: 03-JUN-1997
    APPLICATION NUMBER: US 60/031,930
    FILING DATE: 27-NOV-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965
    REFERENCE/DOCKET NUMBER: 10797-002201 (formerly 3983/59818)
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906
  INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1208 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..651
  SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16

Alignment Scores:
Pred. No.:
Score: Length: 1208
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                       Gaps: 0

US-09-976-740-19 (1-15) x US-08-979-608A-16 (1-1208)

```
Qy    1 GluGluGluLuAspAspAspGluAspGluLuAspGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAAGAAGAATGATGATGATGAAGATGAAGATGAAGAAGATGAT 66
```

RESULT 8
US-09-517-849-16
; Sequence 16, Application US/0951 7849
; Patent No. 6605588
GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
             Lees, Robert S.
             Law, Simon W.
             Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
       TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/517,849
    FILING DATE: 02-Mar-2000
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/979,608
    FILING DATE: 26-NOV-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965
    REFERENCE/DOCKET NUMBER: 10797-003001
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906
  INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1208 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..651
  SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-517-849-16
```

```
US-09-976-740-19 (1-15) x US-09-517-849-16 (1-1208)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
          ||||||||||||||||||||||||||||||||||||||||||||
Db     22 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 66
```

RESULT 9
US-09-616-289-16
; Sequence 16, Application US/09616289
; Patent No. 663923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-616-289-16

Alignment Scores:
Pred. No.:
Score: 0.00105
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

                            Length: 1208
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

```
US-09-976-740-19 (1-15) x US-09-616-289-16 (1-1208)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
          ||||||||||||||||||||||||||||||||||||||||||||
Db     22 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 66
```

RESULT 10
US-09-616-289-45
; Sequence 45, Application US/09616289
; Patent No. 663923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-616-289-45

Alignment Scores:
Pred. No.:
Score: 0.0014
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

                            Length: 1614
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

```
US-09-976-740-19 (1-15) x US-09-616-289-45 (1-1614)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
          ||||||||||||||||||||||||||||||||||||||||||||
Db    985 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 1029
```

RESULT 11
US-09-616-289-50
; Sequence 50, Application US/09616289
; Patent No. 663923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-50

Alignment Scores:
Pred. No.:
Score: 0.0102
Percent Similarity: 82.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

                            Length: 12425
                            Matches: 15
                            Conservative: 0
                            Mismatches: 0
                            Indels: 0
                            Gaps: 0

```
US-09-976-740-19 (1-15) x US-09-616-289-50 (1-12425)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
          ||||||||||||||||||||||||||||||||||||||||||||
Db   4238 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGAT 4282
```

RESULT 12
US-08-431-080-27
Sequence 27, Application US/08431080
Patent No. 5698686
GENERAL INFORMATION:
  APPLICANT: Gottschling, Daniel E.
  APPLICANT: Singer, Miriam S.
  TITLE OF INVENTION: Telomerase Compositions and Methods
  NUMBER OF SEQUENCES: 32
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TEXAS
    COUNTRY: UNITED STATES OF AMERICA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/431,080
    FILING DATE: Concurrently Herewith
    CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 514
    FILING DATE: October 20, 1994
    APPLICATION NUMBER: SN 08/326,781
  ATTORNEY/AGENT INFORMATION:
    NAME: Parker, David L.
    REGISTRATION NUMBER: 32,165
    REFERENCE/DOCKET NUMBER: ARCD:155/PAR
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (512) 418-3000
    TELEFAX: (713) 789-2679
    TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4599 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-08-431-080-27

Alignment Scores:
Pred. No.:   Length: 4599
Score: 0.0688   Matches: 12
Percent Similarity: 73.00   Conservative: 3
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 80.00%   Indels: 0
DB: 89.02%   Gaps: 0

US-09-976-740-19 (1-15) x US-08-431-080-27 (1-4599)

```
Qy    1 GluGluGluGluAspAspAspGluAspGluGluAspAspAsp   15
        |||||||||||||||||||||||||||||||||||||||||||
Db 1231 GAAGAAGAAGAAGATGATGACGAAGACGACGACGACGAAGATGAT 1275
```

RESULT 13
US-08-938-534-27
Sequence 27, Application US/08938534
Patent No. 5916752
GENERAL INFORMATION:
  APPLICANT: Gottschling, Daniel E.
  APPLICANT: Singer, Miriam S.
  TITLE OF INVENTION: Telomerase Compositions and Methods
  NUMBER OF SEQUENCES: 32
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TEXAS
    COUNTRY: UNITED STATES OF AMERICA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/938,534
    FILING DATE: 26-SEP-1997
    CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/431,080
    FILING DATE: October 20, 1994
    APPLICATION NUMBER: SN 08/326,781
  ATTORNEY/AGENT INFORMATION:
    NAME: Parker, David L.
    REGISTRATION NUMBER: 32,165
    REFERENCE/DOCKET NUMBER: ARCD:155/PAR
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (512) 418-3000
    TELEFAX: (713) 789-2679
    TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4599 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-08-938-534-27

Alignment Scores:
Pred. No.:   Length: 4599
Score: 0.0688   Matches: 12
Percent Similarity: 73.00   Conservative: 3
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 80.00%   Indels: 0
DB: 89.02%   Gaps: 0

US-09-976-740-19 (1-15) x US-08-938-534-27 (1-4599)

```
Qy    1 GluGluGluGluAspAspAspGluAspGluGluAspAspAsp   15
        |||||||||||||||||||||||||||||||||||||||||||
Db 1231 GAAGAAGAAGAAGATGATGACGAAGACGACGACGACGAAGATGAT 1275
```

RESULT 14
US-09-345-294-27
Sequence 27, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
  APPLICANT: Gottschling, Daniel E.
  APPLICANT: Singer, Miriam S.
  TITLE OF INVENTION: Telomerase Compositions and Methods
  NUMBER OF SEQUENCES: 32
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TEXAS
    COUNTRY: UNITED STATES OF AMERICA
    ZIP: 77210
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/345,294
    FILING DATE: 30-Jun-1999
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:

```
;         APPLICATION NUMBER: 08/431,080
;         FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;         NAME: Parker, David L.
;         REGISTRATION NUMBER: 32,165
;         REFERENCE/DOCKET NUMBER: ARCD.155/PAR
; TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (512) 418-3000
;         TELEFAX: (713) 789-2679
;         TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 27:
;   SEQUENCE CHARACTERISTICS:
;         LENGTH: 4599 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-345-294-27

Alignment Scores:
Pred. No.:                      0.0688          Length:              4599
Score:                         73.00            Matches:               12
Percent Similarity:           100.00%           Conservative:           3
Best Local Similarity:         80.00%           Mismatches:             0
Query Match:                   89.02%           Indels:                 0
DB:                            4                Gaps:                   0

US-09-976-740-19 (1-15) x US-09-345-294-27 (1-4599)

Qy     1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||
Db  1231 GAAGAAGAAGAAGAAGATGATGACGAAGACGACGAAGACGATGATGAT 1275


RESULT 15
US-09-220-132-66
; Sequence 66, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SEQ ID NO 66
;   LENGTH: 2736
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-66

Alignment Scores:
Pred. No.:                      0.0786          Length:              2736
Score:                         71.00            Matches:               12
Percent Similarity:           100.00%           Conservative:           3
Best Local Similarity:         80.00%           Mismatches:             0
Query Match:                   86.59%           Indels:                 0
DB:                            4                Gaps:                   0

US-09-976-740-19 (1-15) x US-09-220-132-66 (1-2736)

Qy     1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||:::|||::::::|||:::||||
Db  1325 GAAGAAGAGGAGGAGGATGAGGATGAAGATGAAGATGAGGAT 1369


Search completed: March 13, 2004, 04:06:22
Job time : 9.08568 secs
```

OM protein - nucleic search, using frame_plus_p2n model

```
                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:             March 12, 2004, 20:46:42 ; Search time 21.7013 Seconds
                    (without alignments)
                    2544.725 Million cell updates/sec

Title:              US-09-976-740-19
Perfect score:      82
Sequence:           1 EEEEDDDEDEDD 15

Scoring table:      BLOSUM62
                    Xgapop 10.0 , Xgapext 0.5
                    Ygapop 10.0 , Ygapext 0.5
                    Fgapop 6.0  , Fgapext 7.0
                    Delop  6.0  , Delext  7.0

Searched:           2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters:     4865114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :          Published Applications NA:*

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US0997674O/runat 10032004 094549 19588/app_query.fasta_1.1898
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0997674O @CGN 1_712 @runat 10032004 094549_19588
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Published Applications NA:*
1:  /cgn2_6/ptcdata/1/pubpna/US07_PUBCOMB.seq:*
2:  /cgn2_6/ptcdata/1/pubpna/PCT_NEW_PUB.seq:*
3:  /cgn2_6/ptcdata/1/pubpna/US09C_PUBCOMB.seq:*
4:  /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*
5:  /cgn2_6/ptcdata/1/pubpna/US10A_PUBCOMB.seq:*
6:  /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*
7:  /cgn2_6/ptcdata/1/pubpna/PCTUS_PUBCOMB.seq:*
8:  /cgn2_6/ptcdata/1/pubpna/US07_NEW_PUB.seq:*
9:  /cgn2_6/ptcdata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptcdata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptcdata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*
13: /cgn2_6/ptcdata/1/pubpna/US12_PUBCOMB.seq:*
14: /cgn2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptcdata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptcdata/1/pubpna/US60_PUBCOMB.seq:*
```

SUMMARIES

```
Result  Query
No.     Score  Match Length DB   ID       Description
------  -----  ------------ ---- --       -----------
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
 1   82 100.0     45   9   US-09-962-055-30        Sequence 30, Appl
 2   82 100.0     45   9   US-09-976-740-30        Sequence 30, Appl
 3   82 100.0     45  12   US-10-671-242-30        Sequence 30, Appl
 4   82 100.0     45  13   US-10-023-529-30        Sequence 30, Appl
 5   82 100.0     45  13   US-10-023-523-30        Sequence 30, Appl
 6   82 100.0     45  15   US-10-616-187-30        Sequence 30, Appl
 7   82 100.0     78   9   US-09-962-055-31        Sequence 31, Appl
 8   82 100.0     78   9   US-09-976-740-31        Sequence 31, Appl
 9   82 100.0     78  12   US-10-671-242-31        Sequence 31, Appl
10   82 100.0     78  13   US-10-023-529-31        Sequence 31, Appl
11   82 100.0     78  13   US-10-023-523-31        Sequence 31, Appl
12   82 100.0     78  15   US-10-616-187-31        Sequence 31, Appl
13   82 100.0   1208  15   US-10-616-187-31        Sequence 16, Appl
14   82 100.0   1208  12   US-10-671-242-16        Sequence 16, Appl
15   82 100.0   1208  13   US-10-023-523-16        Sequence 16, Appl
16   82 100.0   1208  13   US-10-023-529-16        Sequence 16, Appl
17   82 100.0   1208  15   US-10-616-187-16        Sequence 16, Appl
18   82 100.0   1336  15   US-10-102-806-247       Sequence 247, Appl
19   82 100.0   1336  15   US-10-102-806-247       Sequence 247, Appl
20   82 100.0   1445  10   US-09-945-527-6         Sequence 6, Appli
21   82 100.0   1614   9   US-09-976-740-45        Sequence 45, Appl
22   82 100.0   1614   9   US-09-962-055-45        Sequence 45, Appl
23   82 100.0   1614  13   US-10-023-529-45        Sequence 45, Appl
24   82 100.0   1614  13   US-10-023-523-45        Sequence 45, Appl
25   82 100.0   1614  15   US-10-616-187-45        Sequence 45, Appl
26   82 100.0  12425   9   US-09-976-740-50        Sequence 50, Appl
27   82 100.0  12425  13   US-10-023-523-50        Sequence 50, Appl
28   82 100.0  12425  13   US-10-023-529-50        Sequence 50, Appl
29   82 100.0  12425  13   US-10-023-523-50        Sequence 50, Appl
30   82 100.0  12425  15   US-10-616-187-50        Sequence 50, Appl
31   82  91.5   1474  12   US-10-425-114-14967     Sequence 14967, A
32   82  91.5   1587  12   US-10-424-599-29792     Sequence 29792, A
33   87.8    872   9   US-09-770-445-559       Sequence 559, App
34   87.8    932  12   US-10-425-114-13034     Sequence 13034, A
35   87.8   1284  14   US-10-032-585-6386      Sequence 6386, App
36   86.6    397  12   US-10-424-599-85863     Sequence 85863, A
37   86.6    454   9   US-09-880-107-2462      Sequence 2462, App
38   86.6    454   9   US-09-954-531-1094      Sequence 1094, Ap
39   86.6    913  12   US-10-424-599-27101     Sequence 27101, A
40   86.6   2142   9   US-09-917-800A-1567     Sequence 1567, Ap
41   86.6   2142  15   US-10-191-803-35        Sequence 35, Appl
42   86.6   2463  15   US-10-331-496A-20       Sequence 20, Appl
43   86.6   2739  12   US-10-072-012-241       Sequence 241, App
44   85.4    231  12   US-10-085-783A-7014     Sequence 7014, Ap
45   85.4    231  15   US-10-242-535A-7014     Sequence 7014, Ap
                        70    231
```

ALIGNMENTS

RESULT 1
US-09-962-055-30
Sequence 30, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
          Lees, Robert S.
          Law, Simon W.
          Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                   TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-Nov-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..45
US-09-962-055-30
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
                                       Matches: 15
Percent Similarity: 82.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 9   Gaps: 0

US-09-976-740-19 (1-15) x US-09-962-055-30 (1-45)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGAAGATGAT 45

US-09-976-740-19 (1-15) x US-09-962-055-30 (1-45)

RESULT 2
US-09-976-740-30
; Sequence 30, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; FILE REFERENCE: 10797-004001
; TITLE OF INVENTION: ATHEROSCLEROSIS

RESULT 3
US-10-671-242-30
; Sequence 30, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
                                       Matches: 15
Percent Similarity: 82.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 9   Gaps: 0

US-09-976-740-19 (1-15) x US-10-671-242-30 (1-45)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGAAGATGAT 45

US-09-976-740-19 (1-15) x US-10-671-242-30 (1-45)

RESULT 4
US-10-023-529-30
; Sequence 30, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS

Query Match: 100.00%   Indels: 0
DB: 13   Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-529-30 (1-45)

FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-30

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 13   Mismatches: 0
DB: Indels: 0
                                        Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-529-30 (1-45)

Qy 1 GluGluGluAspAspAspGluAspGluGluAspAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGAAGATGAT 45

RESULT 5
US-10-023-523-30
Sequence 30, Application US/10023523
Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-523-30

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 13   Mismatches: 0
                                        Indels: 0
                                        Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-523-30 (1-45)

RESULT 6
US-10-616-187-30
Sequence 30, Application US/10616187
Publication No. US20040013668A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-187-30

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 15   Mismatches: 0
DB: Indels: 0
                                        Gaps: 0

US-09-976-740-19 (1-15) x US-10-616-187-30 (1-45)

Qy 1 GluGluGluAspAspAspGluAspGluGluAspAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGAAGATGAT 45

RESULT 7
US-09-962-055-31
Sequence 31, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

Alignment Scores:
Pred. No.:
Score: 4.47e-05   Length: 45
Percent Similarity: 82.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
                                        Mismatches: 0

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..78
SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-962-055-31

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGAATGATGAGAATGAAGAGGAAGATGAAGATGAAGAAGATGAT 45

US-09-976-740-19 (1-15) x US-09-962-055-31 (1-78)

Alignment Scores:
Pred. No.:
Score: 82.00   Length: 78
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                                 Gaps: 0
          7.45e-05

RESULT 8
US-09-976-740-31
Sequence 31, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-31

Alignment Scores:
Pred. No.:
Score: 82.00   Length: 78
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                                 Gaps: 0
          7.45e-05

US-09-976-740-19 (1-15) x US-09-976-740-31 (1-78)

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGAATGATGAGAATGAAGAGGAAGATGAAGATGAAGAAGATGAT 45

RESULT 9
US-10-671-242-31
Sequence 31, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
SOFTWARE: FastSEQ for Windows Version 4.0
NUMBER OF SEQ ID NOS: 53

RESULT 10
US-10-023-529-31
Sequence 31, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens

US-10-023-529-31

Alignment Scores:
Pred. No.:
Score: 7.45e-05   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 13   Indels: 0
                                         Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-529-31 (1-78)

Qy 1 GluGluGluAspAspAspGluGluGluAspAspGluGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGAAGAAGATGAAGAAGAAGATGAT 45

RESULT 11
US-10-023-523-31
Sequence 31, Application US/10022523
Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens

US-10-023-523-31

Alignment Scores:
Pred. No.:
Score: 7.45e-05   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 13   Indels: 0
                                         Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-523-31 (1-78)

Qy 1 GluGluGluAspAspAspGluGluGluAspAspGluGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGAAGAAGATGAAGAAGAAGATGAT 45

RESULT 12
US-10-616-187-31
Sequence 31, Application US/10616187
Publication No. US20040013668A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens

US-10-616-187-31

Alignment Scores:
Pred. No.:
Score: 7.45e-05   Length: 78
Percent Similarity: 82.00   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 15   Indels: 0
                                         Gaps: 0

US-09-976-740-19 (1-15) x US-10-616-187-31 (1-78)

Qy 1 GluGluGluAspAspAspGluGluGluAspAspGluGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GAAGAGGAAGAAGATGATGATGAAGAAGAAGATGAAGAAGAAGATGAT 45

RESULT 13
US-09-962-055-16
Sequence 16, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-962-055-16

Alignment Scores:
Pred. No.:
Score: 0.000956
                             82.00
Percent Similarity: 100.00%   Length: 1208
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
DB: 9   Mismatches: 0
                                             Indels: 0
                                             Gaps: 0

US-09-976-740-19 (1-15) x US-09-962-055-16 (1-1208)

Qy 1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 66

RESULT 14
US-09-976-740-19
Sequence 16, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-09-976-740-16

Alignment Scores:
Pred. No.:
Score: 0.000956
                             82.00
Percent Similarity: 100.00%   Length: 1208
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
DB: 9   Mismatches: 0
                                             Indels: 0
                                             Gaps: 0

US-09-976-740-19 (1-15) x US-09-976-740-16 (1-1208)

Qy 1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
       |||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGATGAT 66

RESULT 15
US-10-671-242-16
Sequence 16, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/976,740
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02

DB: 12   Gaps: 0

US-09-976-740-19 (1-15) x US-10-671-242-16 (1-1208)

Qy   1 GluGluGluGluAspAspAspGluAspGluAspAsp 15
           |||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAT 66

Search completed: March 13, 2004, 04:26:13
Job time : 23.7013 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 12, 2004, 19:55:37 ; Search time 226.799 Seconds
     (without alignments)
     1975.018 Million cell updates/sec

Copyright (c) 1993 - 2004 . Compugen Ltd.

GenCore version 5.1.6

Title: US-09-976-740-19
Perfect score: 82
Sequence: 1 EEEEDEDEDEEDD 15

Scoring table:
   BLOSUM62
   Xgapop   10.0 , Xgapext   0.5
   Ygapop   10.0 , Ygapext   0.5
   Fgapop   6.0 , Fgapext   7.0
   Delop   6.0 , Delext   7.0

Searched: 27513289 seqs, 14931090276 residues

Post-processing: Minimum Match 0%
   Maximum Match 100%
   Listing first 45 summaries

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+_p2n.model - DEV-xlp
-MODEL=2/cgn2_1/USPTO_spool_p/US0976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-Q=/cgn2_1/USPTO_spool_p/US0976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0997674 @CGN 1 1.10232 @runat 10032004 094548 19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
   EST:*
   1:   em_estba:*
   2:   em_esthum:*
   3:   em_estin:*
   4:   em_estmu:*
   5:   em_estov:*
   6:   em_estpl:*
   7:   em_estro:*
   8:   em_hc:*
   9:   gb_est1:*
   10:   gb_est2:*
   11:   gb_htc:*
   12:   gb_est3:*
   13:   gb_est4:*
   14:   gb_est5:*
   15:   em_estfun:*
   16:   em_estom:*
   17:   em_gss_hum:*
   18:   em_gss_inv:*
   19:   em_gss_pln:*
   20:   em_gss_vrt:*
   21:   em_gss_nam:*
   22:   em_gss_nam:*
   23:   em_gss_mus:*
   24:   em_gss_pro:*
   25:   em_gss_rod:*
   26:   em_gss_png:*
   27:   em_gss_vrl:*
   28:   gb_gss1:*
   29:   gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	171	9	AA807448	AA807448 nv65b12.s
2	82	100.0	200	10	BE504871	BE504871 hz13g05.x
3	82	100.0	204	9	AA481545	AA481545 aa35g06.s
4	82	100.0	241	9	AI742585	AI742585 wg55g07.x
5	82	100.0	244	9	AA481527	AA481527 aa35e06.s
6	82	100.0	271	9	AA765474	AA765474 oa03d01.s
7	82	100.0	274	12	BI004562	BI004562 MR4-HN005
8	82	100.0	275	9	AA806888	AA806888 oc32g06.s
9	82	100.0	278	9	AA810871	AA810871 ob64g05.s
10	82	100.0	284	9	AA766034	AA766034 oa15b09.s
11	82	100.0	302	10	BF194967	BF194967 701b05.x
12	82	100.0	322	10	AI470106	AI470106 tj99g09.x
13	82	100.0	324	10	BF806978	BF806978 QV4-CI015
14	82	100.0	326	9	AA815219	AA815219 oc0b04.s
15	82	100.0	345	10	BF941758	BF941758 nad2h03.
16	82	100.0	367	9	AA769505	AA769505 nz35b01.s
17	82	100.0	383	10	AW453391	AW453391 CM4-CT004
18	82	100.0	384	10	AA836383	AA836383 od37b07.s
19	82	100.0	397	10	AW594381	AW594381 hg68e08.x
20	82	100.0	412	10	AW134620	AW134620 UI-H-BI1-
21	82	100.0	429	9	AI097526	AI097526 cb87g10.x
22	82	100.0	446	9	AI379283	AI379283 tc73b06.x
23	82	100.0	451	9	AW016794	AW016794 UI-H-BI0p
24	82	100.0	455	9	AI186973	AI186973 qe28f06.x
25	82	100.0	460	9	AW054879	AW054879 ws96a12.x
26	82	100.0	461	9	AI921818	AI921818 wn61e06.x
27	82	100.0	466	10	BF061129	BF061129 7i81c12.x
28	82	100.0	467	9	AI819090	AI819090 wj60h05.x
29	82	100.0	472	9	AI941519	AI941519 wt29g10.x
30	82	100.0	472	9	AA287095	AA287095 zs58e10.s
31	82	100.0	480	9	AI886859	AI886859 wk29e03.x
32	82	100.0	483	9	AI569682	AI569682 tn04d11.x
33	82	100.0	487	9	AI186705	AI186705 qe82e05.x
34	82	100.0	495	9	AI199022	AI199022 qi39g04.x
35	82	100.0	501	9	AI796089	AI796089 wh42c02.x
36	82	100.0	509	9	AI632586	AI632586 wb10g11.x
37	82	100.0	512	10	AW515766	AW515766 hd88b04.x
38	82	100.0	518	10	BE269536	BE269536 601184757
39	82	100.0	572	12	BM697252	BM697252 UI-E-DX0-
40	82	100.0	580	10	BE257093	BE257093 601108824
41	82	100.0	583	9	AI660679	AI660679 wf23e11.x
42	82	100.0	590	9	AI123580	AI123580 qa50b10.x
43	82	100.0	593	9	AI928488	AI928488 wp02e10.x
44	82	100.0	680	10	BE675122	BE675122 7f02h07.x
45	82	100.0	683	10	BE857956	BE857956 7f73a12.x

ALIGNMENTS

RESULT 1
LOCUS   AA807448
AA807448   AA807448   171 bp   mRNA   linear   EST 18-FEB-1998
DEFINITION   nv65b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234655 3'
   similar to contains element MER22 repetitive element ;, mRNA
   sequence.
ACCESSION   AA807448
VERSION   AA807448.1   GI:2877024
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 171)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
              Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: -40m13 fwd. ET from Amersham
              High quality sequence stop: 158.
              Insert Length: 1069   Std Error: 0.00
FEATURES   Location/Qualifiers
     source   1..171
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1234655"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGGAGGCGGCGCCTCATTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-19 (1-15) x AA807448 (1-171)

Alignment Scores:
 Pred. No.:   0.264
 Score: 82.00
 Percent Similarity: 100.00%   Matches: 15   Conservative: 0
 Best Local Similarity: 100.00%   Mismatches: 0   Indels: 0
 Query Match: 9%   Gaps: 0

Qy   1 GluGluGluLeuAspAspAspGluAspGluGluGluAspAsp 15
           |||||||||||||||||||||||||||||||||||||||||
Db   103 GAAGAGGAGAAGAAGATCATGATGAAGAGATGAAGAGAAGATGAT 147

RESULT 2
LOCUS   BE504871
DEFINITION   hz33g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3209816 3',
              similar to contains element TAR1 repetitive element ;, mRNA
              sequence.
ACCESSION   BE504871
VERSION   BE504871.1 GI:9707279
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 200)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
              Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.

LOCUS   BE504871   200 bp   mRNA   linear   EST 04-AUG-2000

REFERENCE   1 (bases 1 to 171)
JOURNAL   Unpublished (1997)
COMMENT   Tumor Gene Index
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
              R. Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL, send email to:
              info@image.llnl.gov
              Seq primer: -40UP from Gibco
              High quality sequence stop: 139.
FEATURES   Location/Qualifiers
     source   1..200
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3209816"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GC6"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (clone IDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-19 (1-15) x BE504871 (1-200)

Alignment Scores:
 Pred. No.:   0.31
 Score: 82.00
 Percent Similarity: 100.00%   Matches: 15   Conservative: 0
 Best Local Similarity: 100.00%   Mismatches: 0   Indels: 0
 Query Match: 10%   Gaps: 0

Qy   1 GluGluGluLeuAspAspAspGluAspGluGluGluAspAsp 15
           |||||||||||||||||||||||||||||||||||||||||
Db   132 GAAGAGGAGAAGAAGATGATGATGAAGAGATGAAGAGAAGATGAT 176

RESULT 3
LOCUS   AA481545
DEFINITION   aa35g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815290 3',
              similar to contains element MER6 repetitive element ;, mRNA
              sequence.
ACCESSION   AA481545
VERSION   AA481545.1 GI:2211097
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 204)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
              Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.

LOCUS   AA481545   204 bp   mRNA   linear   EST 14-AUG-1997

FEATURES   Location/Qualifiers
     source   1..200
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /tissue_type="pooled germ cell tumors"

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution by: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 203.

FEATURES   Location/Qualifiers
source   1..204
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="GDB:6034387"
           /db_xref="taxon:9606"
           /clone="IMAGE:815299"
           /tissue_type="germinal center B cell"
           /lab_host="DH10B"
           /clone_lib="NCI_CGAP_GCB1"
           /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
           polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
           was prepared from human tonsillar cells enriched for
           germinal center B cells by flow sorting (CD20+, IgD-),
           provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
           (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
           primed with a Not I - oligo(dT) primer
           [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3'
           ]. Double-stranded cDNA was ligated to Eco RI adaptors
           (Pharmacia), digested with Not I and cloned into the Not I
           and Eco RI sites of the modified pT7T3 vector. Library
           went through one round of normalization, and was
           constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-19 (1-15) x AA481545 (1-204)

Alignment Scores:
Pred. No.:   0.316
Score: 82.00   Length: 204
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
        |||||||||||||||
Db   104 GAAGAGGAAGAAGGATGATGATGAAGAGGATGAAGAGGATGAAGAGATGAT 148

RESULT 4
LOCUS   AI742585   241 bp   mRNA   linear   EST 19-DEC-1999
DEFINITION   wg55g07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
           IMAGE:2369052 3' similar to contains TAR1.b2 TAR1 TAR1 repetitive
           element ;, mRNA sequence.
ACCESSION   AI742585
VERSION   AI742585.1   GI:5110873
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 241)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tumor Gene Index
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           http://www.ncbi.nlm.nih.gov/ncicgap.
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Insert Length: 901   Std Error: 0.00
           Seq primer: -40UP from Gibco
           High quality sequence stop: 225.

FEATURES   Location/Qualifiers
source   1..241
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="IMAGE:2369052"
           /lab_host="DH10B"
           /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
           /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
           a modified polylinker; Site 1: Not I; Site 2: Eco RI;
           Equal amounts of plasmid DNA from five normalized
           libraries were mixed, and ss circles were made in vitro.
           Following HAP purification, this DNA was used as tracer in
           a subtractive hybridization reaction. The driver was
           PCR-amplified cDNAs from pools of 5,000 clones made from
           the same 5 libraries. The pools consisted of the following
           libraries and cloneID: Soares NbHSF pool 1:
           309384-310919, 323208-325895 Soares Nb2HP pool 1:
           145032-147335, 147720-148103, 148872-149255, 15002 -
           150407, 151176-152327 Soares Nb2HF8-9W pool 1:
           758280-760583, 772104-774407 Soares NbHPA pool 1:
           304776-306311, 320136-322823, 326280-326663 Soares NbHOT
           pool 1: 723720-726407, 739080-740999 Subtraction by Bento
           Soares and M. Fatima Bonaldo."

ORIGIN

US-09-976-740-19 (1-15) x AI742585 (1-241)

Alignment Scores:
Pred. No.:   0.375
Score: 82.00   Length: 241
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
        |||||||||||||||
Db   176 GAAGAGGAAGAAGGATGATGATGAAGAGGATGAAGAGGATGAAGAGATGAT 220

RESULT 5
LOCUS   AA481527   244 bp   mRNA   linear   EST 14-AUG-1997
DEFINITION   aa35e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815266 3',
           similar to contains element MSR1 repetitive element ;, mRNA
           sequence.
ACCESSION   AA481527
VERSION   AA481527.1   GI:2211079
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 244)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
           Ph.D., Gerald Marti, M.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 243.

FEATURES
  source   Location/Qualifiers
                  1..244
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="GDB:6034339"
                  /clone="IMAGE:815266"
                  /db_xref="taxon:9606"
                  /tissue_type="germinal center B cell"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_GCB1"
                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                  polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                  was prepared from human tonsillar cells enriched for
                  germinal center B cells by flow sorting (CD20+, IgD-),
                  provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                  (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                  primed with a Not I - oligo(dT) primer
                  [5'-TGTTACCAATCTGAAGTGGGAGGCGGCCGCCCCTCATTTTTTTTTTTTTTTT-3'
                  ]. Double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Not I and cloned into the Not I
                  and Eco RI sites of the modified pT7T3 vector. Library
                  went through one round of normalization, and was
                  constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Qy   US-09-976-740-19 (1-15) x AA481527 (1-244)

Alignment Scores:
  Pred. No.:   0.38
  Score: 82.00
  Percent Similarity: 100.00%   Matches: 15
  Best Local Similarity: 100.00%   Conservative: 0
  Query Match: 9   Mismatches: 0
  DB: Indels: 0
                                            Gaps: 0

RESULT 6
AA765474
LOCUS   AA765474   271 bp   mRNA   linear   EST 08-FEB-1998
DEFINITION ca03d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303873 3'
            similar to contains Alu repetitive element;contains element MER22
            repetitive element ;, mRNA sequence.
ACCESSION   AA765474
VERSION   AA765474.1 GI:2816712
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Db   101 GAAGAGGAAGAAGAAGATGATGAAGAGATGAAGATGAAGATGAAGAAGATGAT 145

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||
Db   101 GAAGAGGAAGAAGAAGATGATGAAGAGATGAAGATGAAGATGAAGAAGATGAT 145

ORIGIN

FEATURES
  source   Location/Qualifiers
                  1..271
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:1303873"
                  /tissue_type="germinal center B cell"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_GCB1"
                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                  polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                  was prepared from human tonsillar cells enriched for
                  germinal center B cells by flow sorting (CD20+, IgD-),
                  provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                  (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                  primed with a Not I - oligo(dT) primer
                  [5'-TGTTACCAATCTGAAGTGGGAGGCGGCCGCCCCTCATTTTTTTTTTTTTTTT-3'
                  ]. Double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Not I and cloned into the Not I
                  and Eco RI sites of the modified pT7T3 vector. Library
                  went through one round of normalization, and was
                  constructed by Bento Soares and M. Fatima Bonaldo."

Qy   US-09-976-740-19 (1-15) x AA765474 (1-271)

Alignment Scores:
  Pred. No.:   0.424
  Score: 82.00
  Percent Similarity: 100.00%   Matches: 15
  Best Local Similarity: 100.00%   Conservative: 0
  Query Match: 9   Mismatches: 0
  DB: Indels: 0
                                            Gaps: 0

RESULT 7
BI004562/c
BI004562
LOCUS   BI004562   274 bp   mRNA   linear   EST 13-JUN-2001
DEFINITION MR4-HN0054-070301-002-g04 HN0054 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI004562
VERSION   BI004562.1 GI:14408636
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 274)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
  PUBMED   10737800
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR4&t2=MR4-HN0054-
            070301-002-g04&t3=2001-03-07&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 39

Db   82 GAAGAGGAAGAAGAAGATGATGAAGAGATGAAGATGAAGATGAAGAAGATGAT 126

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
         |||||||||||||||||||||||||||||||||||||||
Db   82 GAAGAGGAAGAAGAAGATGATGAAGAGATGAAGATGAAGATGAAGAAGATGAT 126

REFERENCE   1 (bases 1 to 271)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1136 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 269.

FEATURES
    source   High quality sequence stop: 274.
               Location/Qualifiers
               1..274
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_lib="HN0054"
               /note="Organ: head normal; Vector: puc18; Site 1: SmaI;
               Site 2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               into the pUC 18 vector. Reverse transcription of
               profiles into low stringency mRNA and cDNA amplification were performed under
               low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.:   0.428
Score: 82.00
Percent Similarity: 100.00%   Length: 274
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
DB: 12   Mismatches: 0
                               Indels: 0
                               Gaps: 0

US-09-976-740-19 (1-15) x BI004562 (1-274)

Qy   1 GluGluGluGluAspAspGluAspGluGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||||||
Db 251 GAAGAGGAAGAAGATGATGATGATGAAGATGAAGATGAGGAAGAGGAAGATGAT 207

RESULT 8
LOCUS   AA806888   275 bp   mRNA   linear   EST 07-APR-1998
DEFINITION   oc32g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351450 3',
           similar to contains element TAR1 repetitive element ;, mRNA
           sequence.
ACCESSION   AA806888
VERSION   AA806888.1   GI:2876464
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 275)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
           Ph.D., Gerald Marti, M.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Insert Length: 1112   Std Error: 0.00
           Seq primer: -40m13 fwd ET from Amersham
           High quality sequence stop: 229.
FEATURES
    source   Location/Qualifiers
               1..275
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1351450"
               /tissue_type="germinal center B cell"
               /lab_host="DH10B"
               /clone_lib="NCI_CGAP_GCB1"
               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
               polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

ORIGIN
      polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
      was prepared from human tonsillar cells enriched for
      germinal center B cells by flow sorting (CD20+, IgD-),
      provied by Dr. Louis M. Staudt (NCI), Dr. David Allman
      (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
      primed with a Not I - oligo(dT) primer
      [5'-TGTTACCAATCTGAAGTGGGACGCGGCGCCCTCATTTTTTTTTTTTTTT-3',
      ]. Double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization, and was
      constructed by Bento Soares and M. Fatima Bonaldo."

Alignment Scores:
Pred. No.:   0.43
Score: 82.00
Percent Similarity: 100.00%   Length: 275
Best Local Similarity: 100.00%   Matches: 15
Query Match: 100.00%   Conservative: 0
DB: 9   Mismatches: 0
                                 Indels: 0
                                 Gaps: 0

US-09-976-740-19 (1-15) x AA806888 (1-275)

Qy   1 GluGluGluGluAspAspGluAspGluGluGluAspAsp 15
        |||||||||||||||||||||||||||||||||||||||
Db   85 GAAGAGGAAGAAGATGATGATGATGAAGATGAAGATGAGGAAGAGGAAGATGAT 129

RESULT 9
LOCUS   AA810871   278 bp   mRNA   linear   EST 19-FEB-1998
DEFINITION   cb64g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336184 3',
           similar to contains element PIR7 repetitive element ;, mRNA
           sequence.
ACCESSION   AA810871
VERSION   AA810871.1   GI:2880482
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 278)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
           Ph.D., Gerald Marti, M.D.
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Insert Length: 1143   Std Error: 0.00
           Seq primer: -40m13 fwd ET from Amersham
           High quality sequence stop: 269.
FEATURES
    source   Location/Qualifiers
               1..278
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1336184"
               /tissue_type="germinal center B cell"
               /lab_host="DH10B"
               /clone_lib="NCI_CGAP_GCB1"
               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
               polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
               was prepared from human tonsillar cells enriched for
               germinal center B cells by flow sorting (CD20+, IgD-),

ORIGIN

[5'-TGTTACCAATCTGAAGTGGGAGGTGGGAGCGCGCGCCGCCCGCCCATTTTTTTTTTTTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

RESULT 10

Alignment Scores:

Pred. No.:
Score:

```
Pred. No.:              0.435
Score:                 82.00
Percent Similarity:   100.00%     Length:       278
Best Local Similarity:100.00%     Matches:       15
Query Match:           9          Conservative:   0
                                  Mismatches:     0
                                  Indels:         0
                                  Gaps:           0
```

US-09-976-740-19 (1-15) x AA810871 (1-278)

```
Qy  1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
       |||||||||||||||
Db 82 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGAATGAT 126
```

Db

LOCUS   AA766034   284 bp   mRNA   linear   EST 08-FEB-1998
DEFINITION oa1sb09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1305017 3',
            similar to contains element MER22 repetitive element ; mRNA
            sequence.
ACCESSION   AA766034
VERSION   AA766034.1 GI:2817272
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 284)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone Distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            Insert Length: 1100   Std Error: 0.00
            High quality sequence stop: 283.

FEATURES   Location/Qualifiers
     source   1..284
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1305017"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer

ORIGIN

[5'-TGTTACCAATCTGAAGTGGGAGGTGGGAGCGCGCGCCGCCCGCCCATTTTTTTTTTTTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

RESULT 11

Alignment Scores:

Pred. No.:
Score:

```
Pred. No.:              0.445
Score:                 82.00
Percent Similarity:   100.00%     Length:       284
Best Local Similarity:100.00%     Matches:       15
Query Match:           9          Conservative:   0
                                  Mismatches:     0
                                  Indels:         0
                                  Gaps:           0
```

US-09-976-740-19 (1-15) x AA766034 (1-284)

```
Qy  1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
       |||||||||||||||
Db 81 GAAGAGGAAGAAGAATGATGATGAAGATGAAGATGAAGAAGAATGAT 125
```

Db

LOCUS   BF194967   302 bp   mRNA   linear   EST 03-NOV-2000
DEFINITION 7o91b05.x1 NCI_CGAP Ov18 Homo sapiens cDNA clone IMAGE:3643712 3',
            similar to contains element TAR1 TAR1 repetitive element ; mRNA
            sequence.
ACCESSION   BF194967
VERSION   BF194967.1 GI:11081346
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 302)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
            Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing Center
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov.

FEATURES   Location/Qualifiers
     source   1..302
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3643712"
                     /tissue_type="fibrotheoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NCI_CGAP Ov18"
                     /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5',
                     TGTTACCAATCTGAAGTGGGAGGTGGGAGCGCGCGCCGCCCGCCCGACATTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to the Not I adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:
Score:

```
Pred. No.:              0.474          Length:       302
Score:                 82.00          Matches:       15
```

RESULT 12

```
Qy          1 GluGluGluAspAspAspGluAspGluAspAsp 15
              ||||||||||||||||||||||||||||||||
Db        168 GAAGAGGAAGAAGATGATGATGAAGAGATGAAGAGAGATGAT 212
```

US-09-976-740-19 (1-15) x BF194967 (1-302)

```
Percent Similarity:    100.00%        Conservative:    0
Best Local Similarity: 100.00%        Mismatches:      0
DB:                    10             Indels:          0
                                      Gaps:            0
```

```
LOCUS       AI470106      322 bp    mRNA    linear    EST 14-APR-1999
DEFINITION  tj90g09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2148832 3' similar to contains TAR1.b2 PTR5 repetitive
            element ;, mRNA sequence.
ACCESSION   AI470106
VERSION     AI470106.1  GI:4332196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 322)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
            Insert Length: 387  Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1..322
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2148832"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site 1: Not I; Site 2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     15407, 151176-152327 Soares Nb2H8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1: 723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
ORIGIN
```

US-09-976-740-19 (1-15) x AI470106 (1-322)

```
Alignment Scores:      Score:          0.506    Length:        322
                       Pred. No.:      82.00    Matches:        15
Percent Similarity:    100.00%        Conservative:    0
Best Local Similarity: 100.00%        Mismatches:      0
Query Match:           9              Indels:          0
DB:                                   Gaps:            0
```

```
Qy          1 GluGluGluAspAspAspGluAspGluAspAsp 15
              ||||||||||||||||||||||||||||||||
```

Db   152 GAAGAGGAAGAAGAATGATGATGAAGAGATGAAGAGAGATGAT 196

RESULT 13

```
BF806978                  324 bp    mRNA    linear    EST 12-JAN-2001
DEFINITION  QV4-CI0151-091100-522-a05 CI0151 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF806978
VERSION     BF806978.1  GI:12135967
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   MEDLINE   20202663
    PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL:
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-CI0151-
            091100-522-a05&t3=2000-11-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1..324
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="CI0151"
                     /note="Organ: colon ins; Vector: puc18; Site 1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - the pUC 18 vector. Reverse transcription of
                     profiles into Ludwig Institute for Cancer Research)
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
```

US-09-976-740-19 (1-15) x BF806978 (1-324)

```
Alignment Scores:      Score:          0.509    Length:        324
                       Pred. No.:      82.00    Matches:        15
Percent Similarity:    100.00%        Conservative:    0
Best Local Similarity: 100.00%        Mismatches:      0
Query Match:           10             Indels:          0
DB:                                   Gaps:            0
```

```
Qy          1 GluGluGluAspAspAspGluAspGluAspAsp 15
              ||||||||||||||||||||||||||||||||
Db         47 GAAGAGGAAGAAGATGATGATGAAGAGATGAAGAGAGATGAT 91
```

RESULT 14

```
LOCUS       AA815219                  326 bp    mRNA    linear    EST 05-MAR-1998
DEFINITION  oc05b04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339951 3'
```

ACCESSION   AA815219
VERSION   AA815219.1   GI:2884815
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 326)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
          Ph.D., Gerald Marti, M.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Insert Length: 1568   Std Error: 0.00
          Seq primer: -40m13 fwd. ET from Amersham.
FEATURES   Location/Qualifiers
     source   1..326
                 /organism="Homo sapiens"
                 /mol_type="mRNA"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:1339951"
                 /tissue_type="germinal center B cell"
                 /lab_host="DH10B"
                 /clone_lib="NCI_CGAP_GCB1"
                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                 was prepared from human tonsillar cells enriched for
                 germinal center B cells by flow sorting (CD20+, IgD-),
                 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                 primed with a Not I - oligo(dT) primer
                 [5'-TGTTACCAATCTGAAGTGGGAGGGCGCCCCTCAATTTTTTTTTTTTTTTTTT-3'
                 ]. Double-stranded cDNA was ligated to Eco RI adaptors
                 (Pharmacia), digested with Not I and cloned into the Not I
                 and Eco RI sites of the modified pT7T3 vector. Library
                 went through one round of normalization, and was
                 constructed by Bento Soares and M. Fatima Bonaldo."

US-09-976-740-19 (1-15) x AA815219 (1-326)

Alignment Scores:
Pred. No.:   0.512
Score: 82.00   Length: 326
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 9   Indels: 0
                                     Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
            ||||||||||||||||||||||||||||||||||||
Db   68 GAAGAGGAGAGAAGAATGAGATGATGAAGAAGATGAAGAGAAGATGAT 112

KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
          R. Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento
          Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
          I.M.A.G.E. Consortium DNA Sequencing by: Washington University
          Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL, send email to:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco
          High quality sequence stop: 325.
FEATURES   Location/Qualifiers
     source   1..345
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3433564"
                /tissue_type="fibrotheoma"
                /clone_lib="DH10B (phage-resistant)"
                /lab_host="NCI_CGAP_Ov18"
                /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                TGTTACCAATCTGAAGTGGGAGGGCGGCGCCGACATTTTTTTTTTTTTTTT 3'];
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not
                I and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo. "

US-09-976-740-19 (1-15) x BF941758 (1-345)

Alignment Scores:
Pred. No.:   0.543
Score: 82.00   Length: 345
Percent Similarity: 100.00%   Matches: 15
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 10   Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspAsp 15
            ||||||||||||||||||||||||||||||||||||
Db   159 GAAGAGGAGAGAAGAATGAGATGATGAAGAAGATGAAGAGAAGATGAT 203

RESULT 15
LOCUS   BF941758   345 bp   mRNA   linear   EST 30-MAR-2001
DEFINITION   nad92h03.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3433564 3'
          sequence.
          similar to contains element PTR5 repetitive element ;, mRNA
ACCESSION   BF941758
VERSION   BF941758.1   GI:12359078

Search completed: March 13, 2004, 04:01:36
Job time : 232.799 secs

OM protein - nucleic search, using frame_plus_p2n model

```
                                      GenCore version 5.1.6
                                      Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:              March 12, 2004, 19:49:56 ; Search time 394.901 Seconds
                                                (without alignments)
                                                2853.675 Million cell updates/sec

Title:               US-09-976-740-20
Perfect score:       136
Sequence:            1 EEEEDDDEDEDEEDDVSEGSEVPESD 26

Scoring table:       BLOSUM62
                     Xgapop 10.0 , Xgapext  0.5
                     Ygapop 10.0 , Ygapext  0.5
                     Fgapop  6.0 , Fgapext  7.0
                     Delop   6.0 , Delext   7.0

Searched:            3470272 seqs, 2167151699S residues

Total number of hits satisfying chosen parameters:    6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:     Minimum Match 0%
                     Maximum Match 100%
                     Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_l/USPTO_spool_p/US09976740//runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN-200000000
-USER=US09976740_@CGN_1_9705@runat_10032004_094548_19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :           GenEmbl:*
                     1: gb_ba:*
                     2: gb_htg:*
                     3: gb_in:*
                     4: gb_om:*
                     5: gb_ov:*
                     6: gb_pat:*
                     7: gb_ph:*
                     8: gb_pl:*
                     9: gb_pr:*
                     10: gb_ro:*
                     11: gb_sts:*
                     12: gb_sy:*
                     13: gb_un:*
                     14: gb_vi:*
                     15: gb_ba:*
                     16: gb_fun:*
                     17: em_hum:*
                     18: em_in:*
                     19: em_mu:*
                     20: em_om:*
                     21: em_or:*
                     22: em_ov:*
                     23: em_pat:*
                     24: em_ph:*
                     25: em_pl:*
                     26: em_ro:*
                     27: em_sts:*
                     28: em_un:*
                     29: em_vi:*
                     30: em_htg_hum:*
                     31: em_htg_inv:*
                     32: em_htg_other:*
                     33: em_htg_mus:*
                     34: em_htg_pln:*
                     35: em_htg_rod:*
                     36: em_htg_mam:*
                     37: em_htg_vrt:*
                     38: em_sy:*
                     39: em_htgo_hum:*
                     40: em_htgo_mus:*
                     41: em_htgo_other:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB ID	Description
1	136	100.0	78	6	AR199539	AR199539 Sequence
2	136	100.0	78	6	AR374691	AR374691 Sequence
3	136	100.0	78	6	AR409326	AR409326 Sequence
4	136	100.0	78	6	AX239588	AX239588 Sequence
5	136	100.0	78	6	BD056453	BD056453 Novel low
6	136	100.0	982	9	BC007384	BC007384 Homo sapi
7	136	100.0	1208	6	AR199535	AR199535 Sequence
8	136	100.0	1208	6	AR374687	AR374687 Sequence
9	136	100.0	1208	6	AR409322	AR409322 Sequence
10	136	100.0	1208	6	AX239573	AX239573 Sequence
11	136	100.0	1208	6	BD056449	BD056449 Novel low
12	136	100.0	1470	6	BC030129	BC030129 Homo sapi
13	136	100.0	1614	6	AR409337	AR409337 Sequence
14	136	100.0	1614	6	AX239602	AX239602 Sequence
15	136	100.0	1617	9	AY453840	AY453840 Homo sapi
16	136	100.0	12425	6	AR409341	AR409341 Sequence
17	136	100.0	12425	6	AX239607	AX239607 Sequence
18	100.0	237931	9	AC022098	AC022098 Homo sapi
19	116	85.3	140795	2	AC079562	AC079562 Mus muscu
20	116	85.3	218687	2	AC079501	AC079501 Mus muscu
21	108	79.4	215265	2	AC134005	AC134005 Rattus no
22	108	79.4	263957	2	AC120697	AC120697 Rattus no
23	108	79.4	279020	2	AC133803	AC133803 Rattus no
24	104.5	76.8	84	6	AR199545	AR199545 Sequence
25	104.5	76.8	84	6	AR374697	AR374697 Sequence
26	104.5	76.8	84	6	AR409332	AR409332 Sequence
27	104.5	76.8	84	6	AX239594	AX239594 Sequence
28	104.5	76.8	84	6	BD056459	BD056459 Novel low
29	104.5	76.8	1362	6	AR199531	AR199531 Sequence
30	104.5	76.8	1362	6	AR374683	AR374683 Sequence
31	104.5	76.8	1362	6	AR409318	AR409318 Sequence
32	104.5	76.8	1362	6	AX239569	AX239569 Sequence
33	104.5	76.8	1362	6	BD056445	BD056445 Novel low
34	104.5	76.8	1422	6	AR199532	AR199532 Sequence
35	104.5	76.8	1422	6	AR374684	AR374684 Sequence
36	104.5	76.8	1422	6	AR409319	AR409319 Sequence
37	104.5	76.8	1422	6	AX239570	AX239570 Sequence
38	104.5	76.8	1422	6	BD056446	BD056446 Novel low
39	104.5	76.8	1617	6	AR199530	AR199530 Sequence
40	104.5	76.8	1617	6	AR374682	AR374682 Sequence
41	104.5	76.8	1617	6	AR409317	AR409317 Sequence
42	104.5	76.8	1617	6	AX239568	AX239568 Sequence
43	104.5	76.8	1617	6	BD056444	BD056444 Novel low
44	104.5	76.8	2560	4	AY453841	AY453841 Oryctolag
45	104.5	76.8	2561	6	AR409339	AR409339 Sequence

RESULT 1

ALIGNMENTS

AR199539
LOCUS   AR199539   78 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 31 from patent US 6355451.
ACCESSION   AR199539
VERSION   AR199539.1 GI:20249613
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 31 12-MAR-2002;
FEATURES   Location/Qualifiers
  source   1..78
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN

US-09-976-740-20 (1-26) x AR199539 (1-78)

Alignment Scores:
Pred. No.:
Score: 136.00   Length: 78
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspGlyAspGluGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGAAGATGTGTCAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78

RESULT 2
AR374691
LOCUS   AR374691   78 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 31 from patent US 6605588.
ACCESSION   AR374691
VERSION   AR374691.1 GI:40077506
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 31 12-AUG-2003;
FEATURES   Location/Qualifiers
  source   1..78
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

US-09-976-740-20 (1-26) x AR374691 (1-78)

Alignment Scores:
Pred. No.:
Score: 136.00   Length: 78
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspGlyAspGluGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGAAGATGTGTCAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78

RESULT 3
AR409326
LOCUS   AR409326   78 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 31 from patent US 6632923.
ACCESSION   AR409326
VERSION   AR409326.1 GI:40160114
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 31 14-OCT-2003;
FEATURES   Location/Qualifiers
  source   1..78
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

US-09-976-740-20 (1-26) x AR409326 (1-78)

Alignment Scores:
Pred. No.:
Score: 136.00   Length: 78
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

Qy   1 GluGluGluGluAspAspGlyAspGluGluAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGAATGATGATGAAGATGAAGAAGATGTGTCAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78

RESULT 4
AX239588
LOCUS   AX239588   78 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION Sequence 31 from Patent WO0164874.
ACCESSION   AX239588
VERSION   AX239588.1 GI:15797264
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in diagnosing
            and treating atherosclerosis
  JOURNAL   Patent: WO 016874-A 31 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
  source   1..78
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN

US-09-976-740-20 (1-26) x AX239588 (1-78)

Alignment Scores:
Pred. No.:
Score: 136.00   Length: 78
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
                                       Indels: 0

DB: US-09-976-740-20 (1-26) x AX239588 (1-78)   6   Gaps: 0

```
Qy   1 GluGluGluGluAspAspAspGluAspGluAspGluAspValSerGluGlySer 20
       ||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGATGTGTCAGAGGGCTCT 60

Qy  21 GluValProGluSerAsp 26
       ||||||||||||
Db  61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 5
BD056453

LOCUS   BD056453   78 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis.
ACCESSION   BD056453
VERSION   BD056453.1 GI:22602059
KEYWORDS   JP 2001506983-A/11.
SOURCE   Aequorea victoria
  ORGANISM Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 78)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 2001506983-A 11 29-MAY-2001;
            BOSTON HEART FOUNDATION INC
PN   JP 2001506983-A/11
PD   29-MAY-2001
PF   26-NOV-1997 JP 199852487 0
PR   27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC
A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC
C07H21/00,
PC   C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC
            Strandedness: Single;
CC   Topology: Linear;
FEATURES   Location/Qualifiers
FH   Key   Location/Qualifiers
     source   1..78
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

US-09-976-740-20 (1-26) x BD056453 (1-78)

Alignment Scores:
Pred. No. :   4.7e-11   Length: 78
Score: 136.00   Matches: 26
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 6   Gaps: 0

```
Qy   1 GluGluGluGluAspAspAspGluAspGluAspGluAspValSerGluGlySer 20
       ||||||||||||||||||||||||||||
Db   1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGATGTGTCAGAGGGCTCT 60

Qy  21 GluValProGluSerAsp 26
       ||||||||||||
Db  61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 6
BC007384

LOCUS   BC007384   982 bp   mRNA   linear   PRI 16-SEP-2003
DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
            IMAGE:3677194), partial cds.
ACCESSION   BC007384
VERSION   BC007384.2 GI:33988219
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 982)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 982)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (01-MAY-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   On Aug 20, 2003 this sequence version replaced gi:13938477.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 24 Row: g Column: 10.
FEATURES   Location/Qualifiers
     source   1..982
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3677194"
                     /tissue_type="Lymph, Burkitt lymphoma"
                     /clone_lib="NIH_MGC_8"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     gene   1..982
                     /gene="LOC90378"
                     /db_xref="LocusID:90378"
     CDS   <1..711
                     /gene="LOC90378"
                     /codon_start=1
                     /product="LOC90378 protein"
                     /protein_id="AAH07384.2"
                     /db_xref="GI:33988220"
                     /db_xref="LocusID:90378"
                     /translation="PGRAPPAASARPSRSKRGGEERVLEKEEEEDDDDEDEEDDVSE

misc_feature

```
/gene="LOC90378"
/note="SAM; Region: Sterile alpha motif. Widespread domain
in signaling and nuclear proteins. In EPH-related
tyrosine kinases, appears to mediate cell-cell initiated
signal transduction via the binding of SH2-containing
proteins to a conserved tyrosine that is phosphorylated.
In many cases mediates homodimerisation"
/db_xref="CDD:smart00454"
```

ORIGIN

```
GSEVPESDRPAGAQHHQLNGERGPQSAKERVKEWTPCGPHQQQDEGRGRPAPGSGTRQV
FSMAAVNKEGGTASVAIGPDSPSPVPLLPPGKPALPGADGTPFGCPPGPGKEKPSDPVEW
TVMDVVEYFTEAGFPEQATAFQEQEIDGKSLLIMQRTDVLTGLSIRLGPALKIYEHHI
KVLQQGHFEDDDPDGFLG"
469..669
```

RESULT 7

```
LOCUS       AR199535                1208 bp    DNA     linear  PAT 20-APR-2002
DEFINITION  Sequence 16 from patent US 6355451.
ACCESSION   AR199535
VERSION     AR199535.1  GI:20249609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6355451-A 16 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
```

US-09-976-740-20 (1-26) x AR199535 (1-1208)

Alignment Scores:
```
Pred. No.:                              5.53e-10
Score:                       136.00
Percent Similarity:          100.00%     Matches:            26
Best Local Similarity:       100.00%     Conservative:        0
Query Match:                 100.00%     Mismatches:          0
DB:                                9      Indels:             0
                                         Gaps:               0
```

```
Qy          21 GluValProGluSerAsp 26
               ||||||||||||||||||
Db         139 GAAGTGCCCCAGAGTGAC 156
```

```
Qy           1 GluGluGluGluAspAspAspGluAspGluGluAspAspGluAspGluGluGlySer 20
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          79 GAAGAGGAAGAAGATGATGAAGATGAGGAAGATGAAGATGAAGATGTGTCAGAGGGGCTCT 138
```

RESULT 8

```
LOCUS       AR374687                1208 bp    DNA     linear  PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6605588.
ACCESSION   AR374687
VERSION     AR374687.1  GI:40077502
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6605588-A 16 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

US-09-976-740-20 (1-26) x AR374687 (1-1208)

Alignment Scores:
```
Pred. No.:                              6.77e-10
Score:                       136.00
Percent Similarity:          100.00%     Matches:            26
Best Local Similarity:       100.00%     Conservative:        0
Query Match:                 100.00%     Mismatches:          0
DB:                                6      Indels:             0
                                         Gaps:               0
```

```
Qy          21 GluValProGluSerAsp 26
               ||||||||||||||||||
Db          82 GAAGTGCCCGAGAGTGAC 99
```

```
Qy           1 GluGluGluGluAspAspAspGluAspGluGluAspAspGluAspGluGluGlySer 20
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          22 GAAGAGGAAGAAGATGATGAAGATGAGGAAGATGAAGATGAAGATGTGTCAGAGGGGCTCT 81
```

RESULT 9

```
LOCUS       AR409322                1208 bp    DNA     linear  PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6632923.
ACCESSION   AR409322
VERSION     AR409322.1  GI:40160110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE     Low density lipoprotein binding proteins and their use in
            diagnosing and treating atherosclerosis
  JOURNAL   Patent: US 6632923-A 16 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..1208
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

US-09-976-740-20 (1-26) x AR409322 (1-1208)

Alignment Scores:
```
Pred. No.:                              6.77e-10
Score:                       136.00
Percent Similarity:          100.00%     Matches:            26
Best Local Similarity:       100.00%     Conservative:        0
Query Match:                 100.00%     Mismatches:          0
DB:                                6      Indels:             0
                                         Gaps:               0
```

```
Qy          21 GluValProGluSerAsp 26
               ||||||||||||||||||
Db          82 GAAGTGCCCGAGAGTGAC 99
```

```
Qy           1 GluGluGluGluAspAspAspGluAspGluGluAspAspGluAspGluGluGlySer 20
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          22 GAAGAGGAAGAAGATGATGAAGATGAGGAAGATGAAGATGAAGATGTGTCAGAGGGGCTCT 81
```

RESULT 10

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

LOCUS   AX239573   1208 bp   DNA   linear   PAT 26-SEP-2001
DEFINITION   Sequence 16 from Patent WO0164874.
ACCESSION   AX239573
VERSION   AX239573.1   GI:15797257
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density liporotein binding proteins and their use in diagnosing
             and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 16 07-SEP-2001;
             Boston Heart Foundation, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1208
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS   <1..654
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC88296.1"
                     /db_xref="GI:15792258"
                     /db_xref="REMTREMBL:CAC88296"
                     /translation="EERVLEKEEEDDDEDEDEDDVSEGSEVVEPESDRPAGAGHHQLN
                     GERGPQSAKERVKEWTPCCGPHQGQDBGRGRPAPGSGTRQVFSMAAMNKEGGTASVATGP
                     DSFSPVPLPFGKPALPGADGTPFGCCPGRKEKPSDPVEWTVMDVVEYFTEAGFPEQAT
                     AFQQEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHHIKVLCQGHHFEDDDPGFLG"
ORIGIN

US-09-976-740-20 (1-26) x AX239573 (1-1208)

Alignment Scores:
Pred. No.:   6.77e-10
Score: 136.00
Percent Similarity: 100.00%   Length: 1208
Best Local Similarity: 100.00%   Matches: 26
Query Match: 100.00%   Conservative: 0
DB: 6   Mismatches: 0
                                      Indels: 0
                                      Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluGluGluAspAspAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAAGATGAAGATGATGTGTCAGAGGGCTCT 81

RESULT 11

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

LOCUS   BD056449   1208 bp   DNA   linear   PAT 27-AUG-2002
DEFINITION   Novel low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis,.
ACCESSION   BD056449
VERSION   BD056449.1   GI:22602055
KEYWORDS   JP 200150698-A/7.
SOURCE   Aequorea victoria
  ORGANISM   Aequorea victoria
             Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
             Aequoreidae; Aequorea.
REFERENCE   1 (bases 1 to 1208)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Novel low density lipoprotein binding proteins and their use in
             diagnosing and treating atherosclerosis
  JOURNAL   Patent: JP 200150698-A 7 29-MAY-2001;

COMMENT   BOSTON HEART FOUNDATION INC
             PN   JP 200150698-A/7
             PD   29-MAY-2001
             PF   26-NOV-1997
             PR   27-NOV-1996 US   JP 199852870
             PR   26-NOV-1997 US   60/031930,03-JUN-1997 US   60/048547 PI
             ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC
             A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
             C07H21/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
             C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
             Strandedness: Single;
             CC   Topology: Linear;
             FH   Key   Location/Qualifiers
FEATURES   Location/Qualifiers
     source   1..1208
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

US-09-976-740-20 (1-26) x BD056449 (1-1208)

Alignment Scores:
Pred. No.:   6.77e-10
Score: 136.00
Percent Similarity: 100.00%   Length: 1208
Best Local Similarity: 100.00%   Matches: 26
Query Match: 100.00%   Conservative: 0
DB: 6   Mismatches: 0
                                      Indels: 0
                                      Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluGluGluAspAspAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAAGATGAAGATGATGTGTCAGAGGGCTCT 81

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

RESULT 12

LOCUS   BC030129   1470 bp   mRNA   linear   PRI 16-SEP-2003
DEFINITION   Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
             IMAGE:3943601), partial cds.
ACCESSION   BC030129
VERSION   BC030129.2   GI:33871478
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1470)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
             McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
             Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
             Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
             Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
             Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
             Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE   22388257
   PUBMED   12477932

US-09-976-740-20 (1-26) x BC030129 (1-1208)

Alignment Scores:
Pred. No.:   6.77e-10
Score: 136.00
Percent Similarity: 100.00%   Length: 1208
Best Local Similarity: 100.00%   Matches: 26
Query Match: 100.00%   Conservative: 0
DB: 6   Mismatches: 0
                                      Indels: 0
                                      Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluGluGluAspAspAspAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAAGATGAAGATGATGTGTCAGAGGGCTCT 81

Qy   21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

REFERENCE 2 (bases 1 to 1470)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT On Aug 19, 2003 this sequence version replaced gi:22539615.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DPP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
 Hansen,N., Ho,S.-L, Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
 Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
 McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAL Plate: 15 Row: m Column: 17
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Genomescan gene prediction.

FEATURES Location/Qualifiers
 source 1..1470
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:3943601"
  /tissue_type="Lung, small cell carcinoma"
  /clone_lib="NIH_MGC_7"
  /lab_host="DH10B-R"
  /note="Vector: pOTB7"
 gene 1..1470
  /gene="LOC90378"
  /db_xref="LocusID:90378"
 CDS <1..890
  /gene="LOC90378"
  /codon_start=3
  /product="LOC90378 protein"
  /protein_id="AAH30129.1"
  /db_xref="GI:33871479"
  /db_xref="LocusID:90378"
  /translation="GAARPVSLREVVRVLGGSGGAGRLTRGRVQGLLEEAAAARGRL
  ERTRLGALLALPRGDRDRPGRAPPAASARPSRSRKRGGEERVLEKEEEDEDEDEEDDVS
  EGSEVPESDRPAGAQHQLNGRGRPQSAKERVKEWTFCGPHQGQDEGRGRPAPGSGTRQ
  VFSAAMNKEGGTASVAVGPDSPSPVDLPPGKPALPGADGTPFGCPPGCPPGRKKPSDPVE
  WTVMDVVEYFTEAGFFEPQOATAFQEEQEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHH
  IKVLQQGHPEDDPDGPLG"
 misc_feature 648..848
  /gene="LOC90378"
  /note="SAM; Region: Sterile alpha motif. Widespread domain
  in signaling and nuclear proteins. In EPH-related
  tyrosine kinases, appears to mediate cell-cell initiated
  signal transduction via the binding of SH2-containing
  proteins to a conserved tyrosine that is phosphorylated.
  In many cases mediates homodimerisation"
  /db_xref="CD:smart00454"

ORIGIN
 Alignment Scores:
 Pred. No.:

 8.19e-10 Length: 1470

Score: 136.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-976-740-20 (1-26) x BC030129 (1-1470)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluGluGluAspAspValSerGluGlySer 20
  ||||||||||||||||||||||||||
Db 258 GAAGAGGAGGAAGAAGATGATGATGAAGATGAAGAAGAAGAAGATGATGTCAGAGGGCTCT 317

Qy 21 GluValProGluSerAsp 26
  ||||||||||||||||||
Db 318 GAAGTGCCCGAGAGTGAC 335

RESULT 13
AR409337
LOCUS AR409337 1614 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 45 from patent US 6632923.
ACCESSION AR409337
VERSION AR409337.1 GI:40160125
KEYWORDS .
SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE Low density lipoprotein binding proteins and their use in
 diagnosing and treating atherosclerosis
JOURNAL Patent: US 6632923-A 45 14-OCT-2003;
FEATURES Location/Qualifiers
 source 1..1614
  /organism="unknown"
  /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.:

Score: 136.00 8.96e-10 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-976-740-20 (1-26) x AR409337 (1-1614)

Qy 1 GluGluGluGluAspAspAspGluAspGluGluGluGluAspAspValSerGluGlySer 20
  ||||||||||||||||||||||||||
Db 985 GAAGAGGAGGAAGAAGATGATGATGAAGATGAAGAAGAAGAAGATGATGTCAGAGGGCTCT 1044

Qy 21 GluValProGluSerAsp 26
  ||||||||||||||||||
Db 1045 GAAGTGCCCGAGAGTGAC 1062

RESULT 14
AX239602
LOCUS AX239602 1614 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 45 from Patent WO0164874.
ACCESSION AX239602
VERSION AX239602.1 GI:15972275
KEYWORDS .
SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE Low density lipoprotein binding proteins and their use in diagnosing
 and treating atherosclerosis
JOURNAL Patent: WO 0164874-A 45 07-SEP-2001;
 Boston Heart Foundation, Inc. (US)
FEATURES Location/Qualifiers

Left column

```
             source          1..1614
                             /organism="Homo sapiens"
                             /mol_type="unassigned DNA"
                             /db_xref="taxon:9606"
             CDS             1..>1614
                             /note="unnamed protein product"
                             /codon_start=1
                             /protein_id="CAC88299.1"
                             /db_xref="GI:15797276"
                             /db_xref="REMTREMBL:CAC88299"
                             /translation="MAGPPALPPPETAAAITAAAATTAAAASSSAASPHYQEWILDTIDSLRS
             RKARPDLERICRMVRRHGPEPERTRAELEKLIQQRAVLRVSYKGSISYRNAARVQPP
             RRGATPPAPPRAPRGAPAAAAAAAPPTPAPPPPPAPVAAAAPARAPRAAAAATAPP
             SPGPAQPGPRAQRRAAPLAAPPPAPPAVVAPPAGPRRAPPAAPPPAVVAAREPPLPPPQPP
             APPQQOQPPPQPQPPEGGAVRAGGAARPVSLREVVRYLGGGSGGAGGRLTRGRVQGL
             LEEEAAARGRLERTRLGALALPRGDRPGRAPPAASARPSRSKRGGEERVLEKEEEEDD
             DEDEDEDDVSEGSEVPESDRPAGAQHHQLNGERGPQSAKERVKEWTPCGPHQQGDEG
             RGPAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPFGKPALPGADGTPFGCPP
             GRKEKPSDPVEWTWMDVVEYFTEAGFPEQOATAPCQEEIDGKSLLLMQRTDVLTGLSIR
             LGPALKIYEHHIKVLQQGHFEDDDPDGFLG"
             ORIGIN
```

Alignment Scores:

Pred. No.:		
Score:	8.96e-10	Length: 1614
Percent Similarity:	136.00	Matches: 26
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
		Indels: 0
DB:		Gaps: 0

```
US-09-976-740-20 (1-26) x AX239602 (1-1614)

Qy    1 GluGluGluuAspAspAspGluuAspGluuAspGluGluAspAspValSerGluGlySer 20
          |||||||||||||||||||||||||||||
Db  985 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGATGTCAGAGGGGCTCT 1044

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||
Db 1045 GAAGTCCCCGAGAGTGAC 1062
```

Right column

```
                             /codon_start=1
                             /product="atherin"
                             /protein_id="AAR24087.1"
                             /db_xref="GI:38565529"
                             /translation="MAGPPALPPPETAAAITAAAATTAAAASSSAASPHYQEWILDTIDSLRS
             RKARPDLERICRMVRRHGPEPERTRAELEKLIQQRAVLRVSYKGSISYRNAARVQPP
             RRGATPPAPPRAPRGAPAAAAAAAPPTPAPPPPPAPVAAAAPARAPRAAAAATAPP
             SPGPAQPGPRAQRRAAPLAAPPPAPPAVVAPPAGPRRAPPAAPPPAVVAAREPPLPPPQPP
             APPQQOQPPPQPQPPEGGAVRAGGAARPVSLREVVRYLGGGSGGAGGRLTRGRVQGL
             LEEEAAARGRLERTRLGALALPRGDRPGRAPPAASARPSRSKRGGEERVLEKEEEEDD
             DEDEDEDDVSEGSEVPESDRPAGAQHHQLNGERGPQSAKERVKEWTPCGPHQQGDEG
             RGPAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVPLPFGKPALPGADGTPFGCPP
             GRKEKPSDPVEWTWMDVVEYFTEAGFPEQOATAPCQEEIDGKSLLLMQRTDVLTGLSIR
             LGPALKIYEHHIKVLQQGHFEDDDPDGFLG"
             ORIGIN
```

Alignment Scores:

Pred. No.:		
Score:	8.98e-10	Length: 1617
Percent Similarity:	136.00	Matches: 26
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
		Indels: 0
DB:		Gaps: 0

```
US-09-976-740-20 (1-26) x AY453840 (1-1617)

Qy    1 GluGluGluuAspAspAspGluuAspGluuAspGluGluAspAspValSerGluGlySer 20
          |||||||||||||||||||||||||||||
Db  985 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATGATGTCAGAGGGGCTCT 1044

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||
Db 1045 GAAGTCCCCGAGAGTGAC 1062
```

Search completed: March 13, 2004, 00:35:26
Job time : 396.901 secs

```
             RESULT 15
             LOCUS           AY453840                1617 bp    mRNA    linear    PRI 03-DEC-2003
             DEFINITION      Homo sapiens atherin mRNA, complete cds.
             ACCESSION       AY453840
             VERSION         AY453840.1  GI:38565528
             KEYWORDS
             SOURCE          Homo sapiens (human)
               ORGANISM      Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             REFERENCE       1  (bases 1 to 1617)
               AUTHORS       Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
               TITLE         Atherin, a newly identified LDL-binding protein in human
                             atherosclerotic lesions
               JOURNAL       Unpublished
             REFERENCE       2  (bases 1 to 1617)
               AUTHORS       Deconinck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
               TITLE         Direct Submission
               JOURNAL       Submitted (30-OCT-2003) Harvard-MIT Division of Health Sciences and
                             Technology, Boston Heart Foundation, 139 Main Street, Cambridge, MA
                             02142, USA
             FEATURES             Location/Qualifiers
             source          1..1617
                             /organism="Homo sapiens"
                             /mol_type="mRNA"
                             /db_xref="taxon:9606"
                             /chromosome="19"
                             /map="19p13.12"
                             /tissue_type="aorta; liver; fetal brain"
             CDS             1..1617
                             /note="LDL-binding protein; co-localizes with LDL in very
                             early human atherosclerotic lesions"
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: March 12, 2004, 19:48:14 ; Search time 41.2118 Seconds
(without alignments)
2680.137 Million cell updates/sec

Title: US-09-976-740-20
Perfect score: 136
Sequence: 1 EEEEDDDDEDEDEDDVSEGSEVEPESD 26

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5	
Ygapop	10.0	Ygapext	0.5	
Fgapop	6.0	Fgapext	7.0	
Delop	6.0	Delext	7.0	

Searched: 373863 seqs, 212409904l residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
Database :   N Geneseq 29Jan04 :*
1:    geneseqn1980s:*
2:    geneseqn1990s:*
3:    geneseqn2000s:*
4:    geneseqn2001as:*
5:    geneseqn2001bs:*
6:    geneseqn2002s:*
7:    geneseqn2003as:*
8:    geneseqn2003bs:*
9:    geneseqn2003cs:*
10:   geneseqn2004s:*

-MODEL=frame+_p2n.model -DEV=lp
-Q=/cgn2_1/USPTO_spool_p/US00997674O/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFIX=rng -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOCOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000O
-MODE=LOCAL -OUTFMT=pto
-USER=US00997674O @CGN_1_1.1596 @runat_10032004_094547_19532 -NCPU=3
-NO_MMAP -LARGEQUERY_NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	136	100.0	78	5	AAH26503	Low densi
2	136	100.0	1208	2	AAV32838	Human low
3	136	100.0	1208	5	AAH26494	Human low
4	136	100.0	1336	3	AAF21860	Human bre
5	136	100.0	1614	5	AAH26499	Human low
6	136	100.0	12425	5	AAH26495	Human low
7	104.5	76.8	84	5	AAH26509	Low densi
8	104.5	76.8	1362	5	AAH26489	Rabbit lo

9	104.5	76.8	1422	5	AAH26490	Rabbit lo
10	104.5	76.8	1617	2	AAV32835	Rabbit lo
11	104.5	76.8	1617	5	AAH26488	Rabbit lo
12	104.8	76.8	2561	5	AAH26500	Rabbit lo
13	88	64.7	415	8	ACH46971	Human inf
14	88	64.7	421	8	ACH12859	Human adu
15	88	64.7	489	2	AAQ34771	pCENP-B-1
16	88	64.7	500	3	ACH17097	Human can
17	88	64.7	1446	2	AAC77994	Human col
18	88	64.7	1840	5	AAH34498	Human ner
19	88	64.7	2633	5	ABA20783	Human ner
20	88	64.7	2643	5	ABA20784	Human ner
21	88	64.7	3717	2	AAQ39212	CENP-B cd
22	86	63.2	3717	3	ACH22667	Human adu
23	83	61.4	472	5	AAA64660	DNA encod
24	83.5	61.4	468	3	AC37832	Arabidops
25	83.5	61.4	756	6	ABN99215	Arabidops
26	83.5	61.4	921	6	ABZ14690	Arabidops
27	83.5	61.4	1147	3	AAC41072	Arabidops
28	83.5	61.4	1212	4	AAF80353	Nucleotid
29	83	61.0	185	4	ABA73651	Human foe
30	83	61.0	185	4	AAI54090	Probe #22
31	83	61.0	185	4	ABA38881	Probe #17
32	83	61.0	185	4	AAK48265	Human bon
33	83	61.0	185	4	AAK22098	Human bra
34	83	61.0	185	6	ABS47968	Human liv
35	83	61.0	185	6	ABS22132	Human gen
36	83	61.0	547	3	AAA59493	3' sequen
37	83	61.0	578	4	ABA60929	Human foe
38	83	61.0	578	4	AAI40824	Human foe
39	83	61.0	578	4	ABA28903	Probe #95
40	83	61.0	578	4	AAK35108	Human bon
41	83	61.0	578	6	AAK09219	Human bra
42	83	61.0	578	6	ABS34860	Human liv
43	83	61.0	578	6	ABS09569	Human gen
44	83	61.0	766	4	AAI94390	Human neu
45	83	61.0	1284	6	ABZ32099	Candida a

ALIGNMENTS

RESULT 1
AAH26503

ID   AAH26503 standard; DNA; 78 BP.
XX
AC   AAH26503;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
CS   Mammalia.
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784;
PR   14-JUL-2000; 2000US-0061628.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX
PS   Disclosure; Page 9; 143pp; English.
XX
CC   The present sequence is that of a polynucleotide encoding a fragment of
CC   novel low density lipoprotein binding proteins (LBPs) of the invention
CC   (see AAB82797-820). LBPs are capable of binding to native and methylated
CC   low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
CC   LBPs and their fragments are claimed, as well as expression vectors,
CC   cells and methods of producing the LBPs. Methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   animal at risk for atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP are also claimed,
CC   as are pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions
XX
SQ   Sequence 78 BP; 29 A; 7 C; 29 G; 13 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x AAH26503 (1-78)

Alignment Scores:

Pred. No.:	1	Length:	78
Score:	1.45e-11	Matches:	26
	136.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	5	Gaps:	0
DB:	5		

```
Qy  21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db  61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 2
AAV32838

Db   AAV32838
Qy   21 GluValProGluSerAsp 26

ID   AAV32838 standard; cDNA; 1208 BP.
AC   AAV32838;
XX
DT   09-NOV-1998 (first entry)
XX
DE   Human low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW   receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..654
FT   /*tag= a
FT   misc_feature   22..99
FT   /*tag= b
FT   misc_feature   22..66
FT   /note= "Claim 13"
FT   /*tag= c
FT   misc_feature   22..66
FT   /note= "Claim 12"
FT   /*tag= d
FT   misc_feature   67..99
FT   /note= "Claim 14"
FT   /*tag= e
FT   misc_feature   622..651
FT   /note= "Claim 15"
XX
PN   WO9823282-A1.
PD   04-JUN-1998.
XX
PF   26-NOV-1997; 97WO-US021857.
PR   26-NOV-1997;
PR   27-NOV-1996; 96US-0031930P.

PR   03-JUN-1997; 97US-0048547P.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49041.
XX
CC   Nucleic acid encoding low density lipoprotein binding proteins and
CC   related vectors - transformed cells, proteins, and modulators of binding,
CC   useful for treatment and diagnosis of atherosclerosis and for identifying
CC   subjects at risk.
XX
PS   Claim 9; Fig 16; 47pp; English.
XX
CC   This cDNA clone codes for novel human low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49041). It was isolated by screening human
CC   liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA.
CC   clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
CC   42) are claimed. An abnormality in LBP metabolism or structure is
CC   diagnostic of a risk for atherosclerosis. The invention provides: methods
CC   for determining if an animal is at risk for atherosclerosis (including
CC   prenatal screening); methods for treating atherosclerosis (including gene
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP
XX
SQ   Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

US-09-976-740-20 (1-26) x AAV32838 (1-1208)

Alignment Scores:

Pred. No.:	1	Length:	1208
Score:	2.54e-10	Matches:	26
	136.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	2	Gaps:	0

```
Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspGluGluGluSerGluGlySer 20
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22 GAAGAGGAAGAAGAAGATGAATGATGAAGATGAAGAAGAAGATGAATGTGTCAGAGAGGGCTCT 81

Qy  21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db  82 GAAGTGCCCGAGAGTGAC 99
```

RESULT 3
AAH26494

ID   AAH26494 standard; cDNA; 1208 BP.
AC   AAH26494;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..654
FT   /*tag= a
FT   /partial
XX
PN   WO200164874-A2.
XX

PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-0051764.
PR 14-JUL-2000; 2000US-0061628.
XX
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
PR WPI; 2001-565505/63.
DR P-PSDB; AAB82803.
XX
XX
PS Example 4; Fig 16; 143pp; English.
XX
CC The present sequence is that of a partial cDNA encoding novel human low
CC density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC isolated from human foetal brain, liver and aorta cDNA libraries using
CC rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC acids are among claimed polynucleotides of the invention that encode
CC novel polypeptides capable of binding to native and methylated LDL. Also
CC claimed are isolated LBP polypeptides, and biologically active fragments
CC and analogues of them, as well as expression vectors, cells and methods
CC of producing the LBPs. Methods of determining if an animal is at risk for
CC atherosclerosis, methods for evaluating an agent for use in treating
CC atherosclerosis, and methods for treating a cell having an abnormality in
CC structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC are also claimed.
XX
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:
Score: 2.54e-10
                        136.00   Length: 1208
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 5   Indels: 0
                                        Gaps: 0

US-09-976-740-20 (1-26) x AAH26494 (1-1208)

Qy   1 GluGluGluGluAspAspGluAspGluGluAspAspValSerGluGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAGAAGATGATGTGTCAGAGAGGGCTCT 81

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||||||
Db   82 GAAGTGCCCGAGAGTGAC 99

XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005881.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
PR WPI; 2000-611515/58.
DR P-PSDB; AAB58957.
XX
XX
PS Claim 1; Page 670-671; 1299pp; English.
XX
CC New human breast and ovarian cancer associated gene sequences and the
CC polypeptides encoded by these genes, useful in the prevention, treatment
CC and diagnosis of cancer, immune disorders, cardiovascular disorders and
CC neurological diseases.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis of cancer, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
XX
SQ Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:
Score: 2.83e-10
                        136.00   Length: 1336
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 3   Indels: 0
                                        Gaps: 0

US-09-976-740-20 (1-26) x AAF21860 (1-1336)

Qy   1 GluGluGluGluAspAspGluAspGluGluAspAspValSerGluGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAGAAGATGATGTGTCAGAGAGGGCTCT 153

Qy   21 GluValProGluSerAsp 26
          ||||||||||||||||||
Db   154 GAAGTGCCCGAGAGTGAC 171

RESULT 5
AAH26499
ID AAH26499 standard; DNA; 1614 BP.
XX
AC AAH26499;
XX
DT 12-NOV-2001 (first entry)
XX

XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.
XX
DT 27-MAR-2001 (first entry)
XX
AC AAF21860;
XX
ID AAF21860 standard; DNA; 1336 BP.
AAF21860
RESULT 4

US-09-976-740-20 (1-26) x AAH26494 (1-1208)

Db   82 GAAGTGCCCGAGAGTGAC 99
          ||||||||||||||||||
Qy   21 GluValProGluSerAsp 26

Db   22 GAAGAGGAGAAGAGATGATGAAGATGAAGATGAAGAGAAGATGATGTGTCAGAGAGGGCTCT 81
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1 GluGluGluGluAspAspGluAspGluGluAspAspValSerGluGlySer 20

DB: 5   Gaps: 0
Query Match: 100.00%   Indels: 0
Best Local Similarity: 100.00%   Mismatches: 0
Percent Similarity: 100.00%   Conservative: 0
Score: 136.00   Matches: 26
                        2.54e-10   Length: 1208
Pred. No.:
Alignment Scores:

SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

CC are also claimed.
CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC atherosclerosis, and methods for treating a cell having an abnormality in
CC atherosclerosis, methods for evaluating an agent for use in treating
CC of producing the LBPs. Methods of determining if an animal is at risk for
CC and analogues of them, as well as expression vectors, cells and methods
CC claimed are isolated LBP polypeptides, and biologically active fragments
CC novel polypeptides capable of binding to native and methylated LDL. Also
CC acids are among claimed polynucleotides of the invention that encode
CC AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic
CC rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in
CC isolated from human foetal brain, liver and aorta cDNA libraries using
CC density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were
CC The present sequence is that of a partial cDNA encoding novel human low
XX
PS Example 4; Fig 16; 143pp; English.
XX
XX
DR P-PSDB; AAB82803.
PR WPI; 2001-565505/63.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
XX
PR 14-JUL-2000; 2000US-0061628.
PR 02-MAR-2000; 2000US-0051764.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PD 07-SEP-2001.

KW cardiovascular disorder; wound healing; neurological disease; ds.
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
DE Human, breast cancer; ovarian cancer; cytostatic; immunosuppressive;

DE   Human low density lipoprotein binding protein 2; LBP-2; LDL; human;
XX
DE   Low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO20016474-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0517849.
PR   14-JUL-2000; 2000US-0616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX
PS   Claim 7; Fig 7A; 143pp; English.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
CC   The present sequence is that of the coding region of the human gene (see
CC   also AAH26494) encoding novel human low density lipoprotein binding
CC   protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA
CC   library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the
CC   present sequence differs from that predicted from a cDNA clone (see
CC   AAB82803) in that it contains an additional 321 amino acids at its N-
CC   terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among
CC   claimed polynucleotides of the invention that encode novel polypeptides
CC   capable of binding to native and methylated LDL. Also claimed are
CC   isolated LBP polypeptides and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Methods of determining an agent for use in treating
CC   atherosclerosis, and methods for evaluating an agent for use in treating
CC   atherosclerosis, a cell having an abnormality in
CC   structure or metabolism of LBP are claimed. Pharmaceutical compositions
CC   comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
CC   are also claimed
XX
SQ   Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 3.45e-10
Pred. No.:   136.00
Score: 136.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5

US-09-976-740-20 (1-26) x AAH26499 (1-1614)

Length: 1614
Matches: 26
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Qy   1 GluGluGluGluAspAspAspGluAspGluGluAspGluAspAspValSerGluGlySer 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 GAAGAGGAAGAAGATGATGATGAAGATGAAGAGGATGAAGATGATGTGTCAGAGGGCTCT 1044

Qy   21 GluValProGluSerAsp 26
           ||||||||||||||||||
Db   1045 GAAGTGCCCGAGAGTGAC 1062

DT   12-NOV-2001 (first entry)
XX
DE   Human low density lipoprotein binding protein 2; LBP-2; LDL; human;
DE   Low density lipoprotein binding protein 2 (LBP-2) gene.
XX
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   2832..5153
FT   /*tag= a
FT   exon   2832..3785
FT   /note= "includes introns"
FT   /*tag= b
FT   intron   3786..4207
FT   /*tag= c
FT   exon   4208..4502
FT   /*tag= d
FT   intron   4503..4593
FT   /*tag= e
FT   exon   4594..4694
FT   /*tag= f
FT   intron   4695..4787
FT   /*tag= g
FT   exon   4788..4899
FT   /*tag= h
FT   intron   4900..4994
FT   /*tag= i
FT   exon   4995..5153
FT   /*tag= j
XX
PN   WO20016474-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0517849.
PR   14-JUL-2000; 2000US-0616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX
PS   Example 4; Fig 23; 143pp; English.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
CC   The present sequence is that of genomic DNA encoding novel human low
CC   density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was
CC   isolated from a human genomic library by screening with LBP-2 cDNA (see
CC   AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic
CC   acids are among claimed polynucleotides of the invention that encode
CC   novel polypeptides, termed LBPs, capable of binding to native and
CC   methylated LDL. Also claimed are isolated LBP polypeptides, and
CC   biologically active fragments and analogues of them, as well as
CC   expression vectors, cells and methods of producing the LBPs. Methods of
CC   determining if an agent is at risk for atherosclerosis, methods for
CC   evaluating an agent for use in treating atherosclerosis, and methods for
CC   treating a cell having an abnormality in structure or metabolism of LBP
CC   are claimed. Pharmaceutical compositions comprising an LBP polypeptide or
CC   nucleic acid, and vaccine compositions, are also claimed
XX
SQ   Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   2.92e-09   Length: 12425

Score: 136.00
Percent Similarity: 100.00%   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 5   Indels: 0
                                            Gaps: 0

US-09-976-740-20 (1-26) x AAH26495 (1-12425)

```
Qy     1 GluGluGluGluAspAspAspGluAspGluAspValSerGlyGlySer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  4238 GAAGAGGAAGAAGAAGATGATGATGAAGATGAAGAAGAAGATGATGTGTCAGAGGGGCTCT 4297

Qy    21 GluValProGluSerAsp 26
          ||||||||||||||||||
Db  4298 GAAGTGCCCGAGAGTGAC 4315
```

RESULT 7
AAH26509
ID   AAH26509 standard; DNA; 84 BP.
XX
AC   AAH26509;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Low density lipoprotein binding protein (LBP) polynucleotide.
XX
KW   Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;
KW   antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
XX
OS   Mammalia.
XX
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784.9.
PR   14-JUL-2000; 2000US-0061628.9.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Disclosure; Page 10; 143pp; English.
XX

The present sequence is that of a polynucleotide encoding a fragment of
novel low density lipoprotein binding proteins (LBPs) of the invention
(see AAB2797-820). LBPs are capable of binding to native and methylated
low density lipoproteins (LDLs). Isolated polynucleotides encoding novel
LBPs and their fragments are claimed, as well as expression vectors,
cells and methods of producing the LBPs. Methods of determining if an
animal is at risk for atherosclerosis, methods for evaluating an agent
for use in treating atherosclerosis, and methods for treating a cell
having an abnormality in structure or metabolism of LBP are also claimed,
as are pharmaceutical compositions comprising an LBP polypeptide or
nucleic acid, and vaccine compositions

SQ   Sequence 84 BP; 22 A; 16 C; 40 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 4.82e-07   Length: 84
Percent Similarity: 104.50   Matches: 20
Best Local Similarity: 95.30%   Conservative: 6
Percent Similarity: 74.07%   Mismatches: 0
Query Match: 76.84%   Indels: 1
DB: Gaps: 1

US-09-976-740-20 (1-26) x AAH26509 (1-84)

```
Qy     1 GluGluGluGluAspAspAspGluAspGluAspGlu---ValSerGluGly 19
          :::::::::::::::::::::::::::::::::::::::    :::::::
Db     4 GAGGAGGAGGAGGAGGAGGAAGAGGAAGACGACGACGAGGAGGTCGTGTTCCAGGGGC 63

Qy    20 SerGluValProGluSerAsp 26
          :::::::::::::::::::::
Db    64 TCGGAGGTGCCCGAGAGCGAT 84
```

RESULT 8
AAH26489
ID   AAH26489 standard; cDNA; 1362 BP.
XX
AC   AAH26489;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-0051784.9.
PR   14-JUL-2000; 2000US-0061628.9.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82799.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag= a
FT   /partial
XX

PS   Example 2; Fig 12; 143pp; English.
XX

The present sequence is that of cDNA encoding a portion a portion (see AAB82799) of
novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
was isolated following screening of a rabbit cDNA library for clones
encoding LBPs that bound to both native low density lipoprotein (LDL) and
methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
invention provides claimed polynucleotides encoding novel polypeptides
which are capable of binding to native and methylated LDL, the isolated
polypeptides, termed LBPs, and biologically active fragments and
analogues of them, as well as expression vectors, cells and methods of
producing the LBPs. Also claimed are methods of determining if an animal
is at risk for atherosclerosis, methods for evaluating an agent for use
in treating atherosclerosis, and methods for treating a cell having an
abnormality in structure or metabolism of LBP. Pharmaceutical
compositions comprising an LBP polypeptide or nucleic acid, and vaccine
compositions, are also claimed

SQ   Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 8.91e-06   Length: 1362
                                            Matches: 20

Percent Similarity: 96.30%   Conservative: 6
Best Local Similarity: 74.07%   Mismatches: 0
Query Match: 76.84%   Indels: 1
DB: 5   Gaps: 1

US-09-976-740-20 (1-26) x AAH26489 (1-1362)

```
Qy   1 GluGluGluGluuAspAspAspGluAspGluuAspAsp---ValSerGluGly 19
         ||||||||||||||||||||||||||||| :::|||||
Db  61 GAGGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGTCGTGTCCGAGGGC 120

Qy  20 SerGluValProGluSerAsp 26
         |||||||||||||||||
Db 121 TCGGAGGTGCCCGAGAGCGAT 141
```

RESULT 9

ID AAH26490 standard; cDNA; 1422 BP.
XX
AC AAH26490;
XX
DT 12-NOV-2001 (first entry)
XX
DE Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.
XX
KW Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
KW ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key   Location/Qualifiers
FH
FT CDS   1..955
FT   /*tag= a
FT   /partial
XX
PN WO20016874-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006356.
XX
PR 02-MAR-2000; 2000US-0051789O.
PR 14-JUL-2000; 2000US-0616289.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR WPI; 2001-565505/63.
DR P-PSD3; AAB82800.
XX
PS Example 2; Fig 13; 143pp; English.
XX
CC The present sequence is that of cDNA encoding a portion (see AAB82800) of
CC novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA
CC was isolated following screening of a rabbit cDNA library for clones
CC encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in
CC AAH26491. The invention provides claimed polynucleotides encoding novel
CC polypeptides which are capable of binding to native and methylated LDL,
CC the isolated polypeptides, termed LBPs, and biologically active fragments
CC and analogues of them, as well as expression vectors, cells and methods
CC of producing the LBPs. Also claimed are methods of determining if an
CC animal is at risk for atherosclerosis, and methods for evaluating an agent
CC for use in treating atherosclerosis, and methods for treating a cell
CC having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC compositions, are also claimed

SQ Sequence 1422 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;

Alignment Scores: Length: 1422
Pred. No.: 9.32e-06   Matches: 20
Score: 104.50   Conservative: 6
Percent Similarity: 96.30%   Mismatches: 0
Best Local Similarity: 74.07%   Indels: 1
Query Match: 76.84%   Gaps: 1
DB: 5

US-09-976-740-20 (1-26) x AAH26490 (1-1422)

```
Qy   1 GluGluGluGluuAspAspAspGluAspGluuAspAsp---ValSerGluGly 19
         ||||||||||||||||||||||||||||| :::|||||
Db 121 GAGGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGTCGTGTCCGAGGGC 180

Qy  20 SerGluValProGluSerAsp 26
         |||||||||||||||||
Db 181 TCGGAGGTGCCCGAGAGCGAT 201
```

RESULT 10

ID AAV32835 standard; cDNA; 1617 BP.
XX
AC AAV32835;
XX
DT 09-NOV-1998 (first entry)
XX
DE Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX
KW Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;
KW receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key   Location/Qualifiers
FH
FT CDS   1..954
FT   /*tag= a
FT misc_feature   1..954
FT   /*tag= b
FT   /note= "Claim 5"
FT misc_feature   156..1617
FT   /*tag= c
FT   /note= "Claim 5"
FT misc_feature   156..954
FT   /*tag= d
FT   /note= "Claim 6"
FT misc_feature   196..1617
FT   /*tag= c
FT   /note= "Claim 5"
FT misc_feature   313..396
FT   /*tag= f
FT   /note= "Claim 19"
FT misc_feature   313..360
FT   /*tag= e
FT   /note= "Claim 18"
FT misc_feature   361..396
FT   /*tag= g
FT   /note= "Claim 20"
FT misc_feature   631..660
FT   /*tag= h
FT   /note= "Claim 21"
XX
PN WO9823282-A1.
XX
PD 04-JUN-1998.
XX
PF 26-NOV-1997; 97WO-US021857.
XX
PR 27-NOV-1996; 96US-0031930P.
PR 03-JUN-1997; 97US-0048547P.
XX
PA (BOST-) BOSTON HEART FOUND INC.
XX
PI Lees AM, Lees RS, Law SW, Arjona AA;
XX

DR   WPI; 1998-322455/28.
DR   P-PSDB; AAW49038.
XX
PT   Nucleic acid encoding low density lipoprotein binding proteins and
PT   related vectors - transformed cells, proteins, and modulators of binding,
PT   useful for treatment and diagnosis of atherosclerosis and for identifying
PT   subjects at risk.
XX
PS   Claim 4; Fig 11; 47pp; English.
XX
CC   This cDNA clone codes for novel rabbit low density lipoprotein (LDL)
CC   binding protein LBP-2 (see AAW49038). It was isolated by functional
CC   screening of a cDNA library, produced from balloon-deendothelialised
CC   healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to
CC   bind both native and methyl LDL. cDNA clones (see AAV32834-39) and
CC   encoded rabbit and human LBPs (see AAV49037-42) are claimed. An
CC   abnormality in an aspect of LBP metabolism or structure is diagnostic of
CC   a risk for atherosclerosis. The invention provides: methods for
CC   determining if an animal is at risk for atherosclerosis (e.g. for
CC   prenatal screening); methods for treating atherosclerosis (including gene
CC   therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC   formation of atherosclerotic plaque; and methods for treating a cell
CC   having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC   vaccine compositions are also provided, as well as recombinant vectors
CC   and host cells used to produce recombinant LBP
XX
SQ   Sequence 1617 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x AAV32835 (1-1617)

Alignment Scores:
Pred. No.:
Score: 1.07e-05
Percent Similarity: 104.50
Best Local Similarity: 96.30%
Query Match: 74.07%
DB: 76.84%
                            2

Length: 1617
Matches: 20
Conservative: 6
Mismatches: 0
Indels: 1
Gaps: 1

Qy   1 GluGluGluGluGluAspAspAspGluAspGluAspGluAspGluAspGluAspGluAsp---ValSerGluGly 19
          |||||||||||||||||||||||||||||||::::::||||| ||||||||||
Db   316 GAGGAGGAGGAGGAGGAGGAGAAGACGACGACGACGACGACGTCGTGTCCGAGGGC 375

Qy   20 SerGluValProGluSerAsp 26
          ||||||||||||||||||||||
Db   376 TCGGAGGTGCCCGAGGCGAT 396

RESULT 11
AAH26488
ID   AAH26488 standard; cDNA; 1617 BP.
AC   AAH26488;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
SS.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag=   a
FT   /partial
FT   /note= "includes in-frame stop codon at nucleotides
FT   28..30"
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.

PF   28-FEB-2001; 2001WO-US0063356.
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00615289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82798.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
PS   Example 2; Fig 11; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see AAB82798) of
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
CC   was isolated following screening of a rabbit cDNA library for clones
CC   encoding LBPs that bound to both native low density lipoprotein (LDL) and
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The
CC   invention provides claimed polynucleotides encoding novel polypeptides
CC   which are capable of binding to native and methylated LDL, the isolated
CC   polypeptides, termed LBPs, and biologically active fragments and
CC   analogues of them, as well as expression vectors, cells and methods of
CC   producing the LBPs. Also claimed are methods of determining if an animal
CC   is at risk for atherosclerosis, and methods for treating a cell having an
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 1617 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x AAH26488 (1-1617)

Alignment Scores:
Pred. No.:
Score: 1.07e-05
Percent Similarity: 104.50
Best Local Similarity: 96.30%
Query Match: 74.07%
DB: 76.84%
                            5

Length: 1617
Matches: 20
Conservative: 6
Mismatches: 0
Indels: 1
Gaps: 1

Qy   1 GluGluGluGluGluAspAspAspGluAspGluAspGluAspGluAspGluAspGluAsp---ValSerGluGly 19
          |||||||||||||||||||||||||||||||::::::||||| ||||||||||
Db   316 GAGGAGGAGGAGGAGGAGGAGAAGACGACGACGACGACGACGTCGTGTCCGAGGGC 375

Qy   20 SerGluValProGluSerAsp 26
          ||||||||||||||||||||||
Db   376 TCGGAGGTGCCCGAGGCGAT 396

RESULT 12
AAH26500
ID   AAH26500 standard; cDNA; 2561 BP.
AC   AAH26500;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
SS.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   246..1928
FT   /*tag=   a

```
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US0006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82807.
XX
PS   Claim 4; Fig 2A; 143pp; English.
XX
PT   New isolated low density lipoprotein binding polypeptide for treating,
PT   diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
CC   The present sequence is that of cDNA encoding novel rabbit low density
CC   lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was
CC   isolated following screening of a rabbit cDNA library for clones encoding
CC   LBPs that bound to both native low density lipoprotein (LDL) and methyl
CC   LDL. The invention provides claimed polynucleotides encoding novel
CC   polypeptides which are capable of binding to native and methylated LDL,
CC   the isolated polypeptides, termed LBPs, and biologically active fragments
CC   and analogues of them, as well as expression vectors, cells and methods
CC   of producing the LBPs. Also claimed are methods of determining if an
CC   animal is at risk for atherosclerosis, methods for evaluating an agent
CC   for use in treating atherosclerosis, and methods for treating a cell
CC   having an abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and vaccine
CC   compositions, are also claimed
XX
SQ   Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x AAH26500 (1-2561)
DB:

Alignment Scores:
Pred. No.:              1.73e-05
Score:                  104.50
Percent Similarity:     96.30%
Best Local Similarity:  74.07%
Query Match:            76.84%

                Length:        2561
                Matches:       20
                Conservative:  6
                Mismatches:    0
                Indels:        1
                Gaps:          1

Qy     20 SerGluValProGluSerAsp 26
          |||||||||||||
Db   1260 GAGGAGGAGGAGGAGGAGGAGGAAGAGCCACGAGGACGACGAGCAGCGACGACGAGACGTCGTGTCCGAGGGC 1319

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspAsp--ValSerGluGly 19
          ||||||||||||||||||||||||||||
Db   1320 TCGGAGGTGCCCGAGAGCGAT 1340


RESULT 13
ACH46971
ID   ACH46971 standard; cDNA, 415 BP.
XX
AC   ACH46971;
XX
DT   13-OCT-2003 (first entry)
XX
DE   Human infant brain cDNA #1034.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   US20030073623-A1.
XX
```

```
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA-/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M.C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PS   Claim 1; SEQ ID NO 34183; 44pp; English.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 415 BP; 97 A; 92 C; 146 G; 80 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x ACH46971 (1-415)
DB:

Alignment Scores:
Pred. No.:              0.000577
Score:                  88.00
Percent Similarity:     86.96%
Best Local Similarity:  60.87%
Query Match:            64.71%

                Length:        415
                Matches:       14
                Conservative:  6
                Mismatches:    3
                Indels:        0
                Gaps:          0

Qy     21 GluValPro 23
          |||||||
Db    223 GAGGTGCCT 231

Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspAspValSerGluGlySer 20
          ||||||||||||||||||::|||||:|||||::|||::|||::||:
Db    163 GACCGATGAGGAAGAGGATCGATGAGATGAAGAATGACGACCGATGATGATGAGGAGGAGGATGGTGAT 222


RESULT 14
ACH12859
ID   ACH12859 standard; cDNA, 421 BP.
XX
AC   ACH12859;
XX
DT   13-OCT-2003 (first entry)
XX
DE   Human adult brain cDNA #71.
XX
KW   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW   genome mapping; biodiversity; genetic disorder.
```

XX
OS   Homo sapiens.
XX
PN   US20030073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PI   DRMANAC R T.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PS   Claim 1; SEQ ID NO 71; 44pp; English.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 421 BP; 99 A; 93 C; 147 G; 82 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x ACH12859 (1-421)

Alignment Scores:
Pred. No.:   0.000586
Score: 88.00   Length: 421
Percent Similarity: 86.96%   Matches: 14
Best Local Similarity: 60.87%   Conservative: 6
Query Match: 64.71%   Mismatches: 3
DB: 8   Indels: 0
                 Gaps: 0

```
Qy      1 GluGluGluGluAspPAspPAspGluAspGluAspAspValSerGluGlySer 20
          ::::||||||||:::||||||||||||||:::||||||||||::||||||:::|||
Db    167 GACGAGATGAGGAAGAGGAATGAAGATGATGAGACGACGATGATGATGAGGAGGATGGTGAT 226
```

XX
DE   pCENP-B-1 cDNA.
XX
KW   Centromere protein; antibodies; polypeptide; ss.
XX
OS   Homo sapiens.
XX
PN   JP04334398-A.
XX
PD   20-NOV-1992.
XX
PF   08-MAY-1991; 91JP-00102517.
XX
PR   08-MAY-1991; 91JP-00102517.
XX
PA   (DAIK) DAIKIN KOGYO KK.
XX
PS   WPI; 1993-005542/01.
PT   P-PSDB; AAR30641.
XX
DR   Human centromere antigen polypeptide - for detection of human antibodies
DR   and identification of disease.
XX
PS   Disclosure; Fig 4; 15pp; Japanese.
XX
CC   Total RNA was extracted from Jurkat cells and mRNA was prepd. from it. A
CC   cDNA library was prepd. in lambda gt11. A positive clone was isolated and
CC   analysed by antibody screening. A mutant coding sequence in which the 3'-
CC   terminal sequence was deleted was prepd. and used to prepare a
CC   polypeptide in which the C-terminal end is deleted. Epitopes of the CENP-
CC   B protein were determined. These peptides can be used to detect anti-
CC   human centromere antibodies. The type of diseases of a patient having the
CC   antibody can be exactly classified using the polypeptide
XX
SQ   Sequence 489 BP; 123 A; 90 C; 186 G; 90 T; 0 U; 0 Other;

US-09-976-740-20 (1-26) x AAQ34771 (1-489)

Alignment Scores:
Pred. No.:   0.000685
Score: 88.00   Length: 489
Percent Similarity: 86.96%   Matches: 14
Best Local Similarity: 60.87%   Conservative: 6
Query Match: 64.71%   Mismatches: 3
DB: 2   Indels: 0
                 Gaps: 0

```
Qy      1 GluGluGluGluAspPAspPAspGluAspGluAspAspValSerGluGlySer 20
          ::::||||||||:::|||||||||||||||:::|||||||||||::||||||:::|||
Db    241 GACGATGAGGAAGAGGAATGATGAAGATGATGAGAGTGAAGACCGACGATGATGATGAGGAGGATGGTGAT 300
```

Search completed: March 12, 2004, 21:08:35
Job time : 47.2118 secs

RESULT 15
ID   AAQ34771 standard; cDNA; 489 BP.
XX
AC   AAQ34771;
XX
DT   06-MAY-1993 (first entry)

```
Qy     21 GluValPro 23
          |||||||||
Db    227 GAGGTGCCT 235
```

```
Qy     21 GluValPro 23
          |||||||||
Db    301 GAGGTGCCT 309
```

OM protein - nucleic search, using frame_plus_p2n model

Copyright (c) 1993 - 2004 Compugen Ltd.   GenCore version 5.1.6

Run on: March 12, 2004, 20:05:17 ; Search time 8.81518 Seconds
                     (without alignments)
                     1636.805 Million cell updates/sec

Title: US-09-976-740-20
Perfect score: 136
Sequence: 1 EEEEDDDEDEDEEDDVSEGSEVPESD 26

Scoring table: BLOSUM62
                     Xgapop   10.0 , Xgapext   0.5
                     Ygapop   10.0 , Ygapext   0.5
                     Fgapop   6.0 , Fgapext   7.0
                     Delop   6.0 , Delext   7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09976740/runat_10032004_094549_19564/app_query.fasta_1.1898
-DB=issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-DB=issued_Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09976740 @CGN 1_1_235 @runat_10032004_094549_19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                     1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                     2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                     3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                     4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                     5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                     6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	136	100.0	78	4	US-08-979-608A-31	Sequence 31, Appl
2	136	100.0	78	4	US-09-517-849-31	Sequence 31, Appl
3	136	100.0	78	4	US-09-616-289-31	Sequence 31, Appl
4	136	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appl
5	136	100.0	1208	4	US-09-517-849-16	Sequence 16, Appl
6	136	100.0	1208	4	US-09-616-289-16	Sequence 16, Appl
7	136	100.0	1614	4	US-09-616-289-45	Sequence 45, Appl
8	136	100.0	12425	4	US-09-616-289-50	Sequence 50, Appl
9	104.5	76.8	84	4	US-08-979-608A-37	Sequence 37, Appl
10	104.5	76.8	84	4	US-09-517-849-37	Sequence 37, Appl
11	104.5	76.8	84	4	US-09-616-289-37	Sequence 37, Appl
12	104.5	76.8	1362	4	US-08-979-608A-12	Sequence 12, Appl
13	104.5	76.8	1362	4	US-09-517-849-12	Sequence 12, Appl
14	104.5	76.8	1362	4	US-09-616-289-12	Sequence 12, Appl
15	104.5	76.8	1422	4	US-08-979-608A-13	Sequence 13, Appl
16	104.5	76.8	1422	4	US-09-517-849-13	Sequence 13, Appl
17	104.5	76.8	1422	4	US-09-616-289-13	Sequence 13, Appl
18	104.5	76.8	1617	4	US-08-979-608A-11	Sequence 11, Appl
19	104.5	76.8	1617	4	US-09-517-849-11	Sequence 11, Appl
20	104.5	76.8	2561	4	US-09-616-289-48	Sequence 48, Appl
21	104.5	76.8	2561	4	US-09-616-289-48	Sequence 48, Appl
22	88	64.7	489	1	US-07-879-685B-3	Sequence 3, Appl
23	82	60.3	45	1	US-09-616-289A-30	Sequence 30, Appl
24	82	60.3	45	4	US-09-517-849-30	Sequence 30, Appl
25	82	60.3	45	4	US-09-616-289-30	Sequence 30, Appl
26	81	59.6	2188	1	US-08-865-662F-10	Sequence 10, Appl
27	81	59.6	2188	1	US-08-374-219B-10	Sequence 10, Appl
28	81	59.6	3489	2	US-08-728-323A-1	Sequence 1, Appl
29	81	59.6	3489	4	US-09-298-568-1	Sequence 1, Appli
30	81	59.6	3489	4	US-09-410-399-1	Sequence 1, Appli
31	81	59.6	32207	2	US-08-770-379-20	Sequence 20, Appl
32	81	59.6	32207	4	US-08-757-669A-20	Sequence 20, Appl
33	81	59.6	32207	4	US-09-230-371A-20	Sequence 20, Appl
34	80	58.8	2518	3	US-09-433-699-3	Sequence 3, Appli
35	79	58.1	2295	1	US-08-375-300-3	Sequence 3, Appli
36	79	58.1	2295	1	US-09-177-431-3	Sequence 3, Appli
37	79	58.1	2295	5	PCT-US95-16930-3	Sequence 3, Appli
38	79	58.1	4080	1	US-08-375-300-1	Sequence 1, Appli
39	79	58.1	4080	1	US-09-177-431-1	Sequence 1, Appli
40	79	58.1	4080	5	PCT-US95-16930-1	Sequence 1, Appli
41	79	58.1	7585	4	US-09-418-710-22	Sequence 22, Appli
42	77	56.6	19056	3	US-09-272-032-8	Sequence 8, Appli
43	77	56.6	19056	4	US-09-443-218-8	Sequence 8, Appli
44	76.5	56.2	4599	1	US-08-431-080-27	Sequence 27, Appl
45	76.5	56.2	4599	2	US-08-938-534-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-979-608A-31
Sequence 31, Application US/08979608A
Patent No. 6355451

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.
           Lees, Robert S.
           Law, Simon W.
           Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                    BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                    TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804

COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/979,608A
    FILING DATE: 26-NO. 6355451-1997

PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/048,547
    FILING DATE: 03-JUN-1997
    APPLICATION NUMBER: US 60/031,930
    FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...78
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-08-979-608A-31

Alignment Scores:
Pred. No.:
Score: 7.23e-13   Length: 78
Percent Similarity: 136.00   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
    Gaps: 0

US-09-976-740-20 (1-26) x US-08-979-608A-31 (1-78)

```
Qy  1 GluGluGluLuAspAspAspAspGluAspGluGluLuAspPAspValSerGluGlySer 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGATGTGTCAGAGAGGCTCT 60

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 2
US-09-517-849-31
Sequence 31, Application US/0951849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...78
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-517-849-31

Alignment Scores:
Pred. No.:
Score: 7.23e-13   Length: 78
Percent Similarity: 136.00   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
    Gaps: 0

US-09-976-740-20 (1-26) x US-09-517-849-31 (1-78)

```
Qy  1 GluGluGluLuAspAspAspAspGluAspGluGluLuAspPAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAACATGTGTCAGAGAGGGCTCT 60

Qy 21 GluValProGluSerAsp 26
        ||||||||||||||||||
Db 61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 3
US-09-616-289-31
Sequence 31, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
CURRENT APPLICATION NUMBER: US 09/517,849
CURRENT FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-09-616-289-31

Alignment Scores:
Pred. No.:
Score: 7.23e-13   Length: 78
Percent Similarity: 136.00   Matches: 26
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
    Gaps: 0

US-09-976-740-20 (1-26) x US-09-616-289-31 (1-78)

```
Qy  1 GluGluGluLuAspAspAspAspGluAspGluGluLuAspPAspValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 GAAGAGGAAGAAGATGATGATGAAGATGAAGAAGATGAAGATGTGTCAGAGAGGGCTCT 60
```

```
Qy    21 GluValProGluSerAsp 26
         |||||||||||||||||||
Db    61 GAAGTGCCCGAGAGTGAC 78
```

RESULT 4
US-08-979-608A-16
; Sequence 16, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/979,608A
;   FILING DATE: 26-No. 6355451-1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/048,547
;   FILING DATE: 03-JUN-1997
;   APPLICATION NUMBER: US 60/031,930
;   FILING DATE: 27-NOV-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..651
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16

Alignment Scores:
Pred. No.:
Score: Length: 1208
Percent Similarity: Matches: 26
Best Local Similarity: Conservative: 0
Query Match: Mismatches: 0
DB: Indels: 0
                                          Gaps: 0
Pred. No.:   1.4e-11
Score: 136.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

US-09-976-740-20 (1-26) x US-08-979-608A-16 (1-1208)

Qy   1 GluGluGluAspAspGluAspGluAspGluAspAspValSerGluGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAGAAGAAGATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGTGTCAGAGGGCTCT 81

Qy 21 GluValProGluSerAsp 26
         |||||||||||||
```

```
Db    82 GAAGTGCCCGAGAGTGAC 99
```

RESULT 5
US-09-517-849-16
; Sequence 16, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;   TREATING ATHEROSCLEROSIS
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/517,849
;   FILING DATE: 02-Mar-2000
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/979,608
;   FILING DATE: 26-NOV-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Myers, Louis
;   REGISTRATION NUMBER: 35,965
;   REFERENCE/DOCKET NUMBER: 10797-003001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1208 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 1..651
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-517-849-16

Alignment Scores:
Pred. No.:
Score: Length: 1208
Percent Similarity: Matches: 26
Best Local Similarity: Conservative: 0
Query Match: Mismatches: 0
DB: Indels: 0
                                          Gaps: 0
Pred. No.:   1.4e-11
Score: 136.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

US-09-976-740-20 (1-26) x US-09-517-849-16 (1-1208)

Qy   1 GluGluGluAspAspGluAspGluAspGluAspAspValSerGluGlySer 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 GAAGAGGAGAAGAAGATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGTGTCAGAGGGCTCT 81

Qy 21 GluValProGluSerAsp 26
         |||||||||||||
Db 82 GAAGTGCCCGAGAGTGAC 99
```

RESULT 6
US-09-616-289-16
; Sequence 16, Application US/0961628...

Patent No. 6632923
GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 1079-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)

US-09-616-289-16

US-09-976-740-20 (1-26) x US-09-616-289-16 (1-1208)

Alignment Scores:
Pred. No.:                1.4e-11       Length:          1208
Score:                    136.00        Matches:         26
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

Qy   1 GluGluLeuGluAspAspAspAspGlyAspGluAspAspAspAspProValSerGluGlySer 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22 GAAGAGGAAGAAGAATGAAGATGATGAAGAATGAAGATGATGAAGATGATGTGTCAGAGGGCTCT 81

Qy  21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db  82 GAAGTGCCCGAGAGTGAC 99

RESULT 7
US-09-616-289-45
; Sequence 45, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 1079-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)

US-09-616-289-45

Alignment Scores:
Pred. No.:                1.92e-11      Length:          1614
Score:                    136.00        Matches:         26
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-09-976-740-20 (1-26) x US-09-616-289-45 (1-1614)

Qy   1 GluGluLeuGluAspAspAspAspGlyAspGluAspAspAspAspProValSerGluGlySer 20
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 985 GAAGAGGAAGAAGAATGAAGATGATGAAGAATGAAGATGATGAAGATGATGTGTCAGAGGGCTCT 1044

Qy  21 GluValProGluSerAsp 26
       ||||||||||||||||||
Db 1045 GAAGTGCCCGAGAGTGAC 1062

RESULT 8
US-09-616-289-50
; Sequence 50, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 1079-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12425
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-616-289-50

Alignment Scores:
Pred. No.:                1.75e-10      Length:          12425
Score:                    136.00        Matches:         26
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       4             Gaps:            0

US-09-976-740-20 (1-26) x US-09-616-289-50 (1-12425)

Qy    1 GluGluLeuGluAspAspAspAspGlyAspGluAspAspAspAspProValSerGluGlySer 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4238 GAAGAGGAAGAAGAATGAAGATGATGAAGAATGAAGATGATGAAGATGATGTGTCAGAGGGCTCT 4297

Qy  21 GluValProGluSerAsp 26
         ||||||||||||||||||
Db  4298 GAAGTGCCCGAGAGTGAC 4315

RESULT 9
US-08-979-608A-37
; Sequence 37, Application US/0897960BA
; Patent No. 6355451
  GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
            Lees, Robert S.
            Law, Simon W.
            Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
            BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
            TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US 60/048,547
    FILING DATE: 03-JUN-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/979,608A
    FILING DATE: 26-No. 6355451-1997
    APPLICATION NUMBER: US 60/031,930
    FILING DATE: 27-NOV-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965
    REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906
  INFORMATION FOR SEQ ID NO: 37:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 84 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..84
  SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-979-608A-37:

Alignment Scores:
Pred. No.:
Score:                  3.48e-08
                        104.50          Length:            84
Percent Similarity:     96.30%          Matches:           20
Best Local Similarity:  74.07%          Conservative:      6
Query Match:            76.84%          Mismatches:        0
DB:                     4               Indels:            1
                                        Gaps:              1

US-09-976-740-20 (1-26) x US-08-979-608A-37 (1-84)

Qy  1 GluLeuGluGluAspAspAspGluAspGluGluAspAsp---ValSerGluGly 19
        ||||||||||||||||||||||||||||::::|||  :||||||||||
Db  1 GAGGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGACGTCGTGTCCGAGGGC 63

Qy  20 SerGluValProGluSerAsp 26
        ||||||||||||||||||||
Db  64 TCGGAGGTGCCCGAGACGAT 84

RESULT 10
US-09-517-849-37
; Sequence 37, Application US/0951784.9
; Patent No. 6605588
  GENERAL INFORMATION:
  APPLICANT: Lees, Ann M.
            Lees, Robert S.
            Law, Simon W.
            Arjona, Anibal A.
  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
            BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
            TREATING ATHEROSCLEROSIS
  NUMBER OF SEQUENCES: 42
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/517,849
    FILING DATE: 02-Mar-2000
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/979,608
    FILING DATE: 26-NOV-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Myers, Louis
    REGISTRATION NUMBER: 35,965
    REFERENCE/DOCKET NUMBER: 10797-003001
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906
  INFORMATION FOR SEQ ID NO: 37:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 84 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1..84
  SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-517-849-37

Alignment Scores:
Pred. No.:
Score:                  3.48e-08
                        104.50          Length:            84
Percent Similarity:     96.30%          Matches:           20
Best Local Similarity:  74.07%          Conservative:      6
Query Match:            76.84%          Mismatches:        0
DB:                     4               Indels:            1
                                        Gaps:              1

US-09-976-740-20 (1-26) x US-09-517-849-37 (1-84)

Qy  1 GluLeuGluGluAspAspAspGluAspGluGluAspAsp---ValSerGluGly 19
        |||||||||||||||||||||||||||::::|||  :||||||||||
Db  1 GAGGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGACGTCGTGTCCGAGGGC 63

Qy  20 SerGluValProGluSerAsp 26
        ||||||||||||||||||||
Db  64 TCGGAGGTGCCCGAGACGAT 84

RESULT 11
US-09-616-289-37
; Sequence 37, Application US/0961628.9
; Patent No. 6632923

GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-616-289-37

Alignment Scores:
Pred. No.:              3.48e-08
Score:                  104.50          Length:         84
Percent Similarity:     96.30%          Matches:        20
Best Local Similarity:  74.07%          Conservative:   6
Query Match:            76.84%          Mismatches:     0
                                        Indels:         1
                                        Gaps:           1

US-09-976-740-20 (1-26) x US-09-616-289-37 (1-84)

Qy   1 GluGluGluGluuAspAspAspGluuAspGluGluGluuAspGluuAsp---ValSerGluGly  19
        |||||||||||:::||:::|||:::|||:::||||||:::||:::|:::        |||||
Db   4 GAGGAGGAGGAGGAAGCAGAGGAAGCGACGACGAGGACGACGACCAGTCGTTGTTCCGAGGGC  63

Qy  20 SerGluValProGluSerAsp  26
        ||||||||||||||||||
Db  64 TCGGAGGTGCCCGAGAGCGAT  84

RESULT 12
US-08-979-608A-12
; Sequence 12, Application US/08979608A
; Patent No. 6355451
GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997

---

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..696
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-979-608A-12

Alignment Scores:
Pred. No.:              7.09e-07
Score:                  104.50          Length:         1362
Percent Similarity:     96.30%          Matches:        20
Best Local Similarity:  74.07%          Conservative:   6
Query Match:            76.84%          Mismatches:     0
                                        Indels:         1
                                        Gaps:           1

US-09-976-740-20 (1-26) x US-08-979-608A-12 (1-1362)

Qy   1 GluGluGluGluuAspAspAspGluuAspGluGluGluuAspGluuAsp---ValSerGluGly  19
        |||||||||||:::||:::|||:::|||:::||||||:::||:::|:::        |||||
Db  61 GAGGAGGAGGAGGAAGCAGAGGAAGCGACGACGAGGACGACGACCAGTCGTTGTTCCGAGGGC  120

Qy  20 SerGluValProGluSerAsp  26
        ||||||||||||||||||
Db 121 TCGGAGGTGCCCGAGAGCGAT  141

RESULT 13
US-09-517-849-12
; Sequence 12, Application US/09517849
; Patent No. 6605588
GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:
  NAME: Myers, Louis
  REGISTRATION NUMBER: 35,965
  REFERENCE/DOCKET NUMBER: 10797-003001
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617/542-5070
    TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 12:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1362 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: Coding Sequence
    LOCATION: 1...696
  SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-517-849-12

Alignment Scores:
Pred. No.:
Score:                  7.09e-07        Length:         1362
Percent Similarity:     104.50          Matches:        20
Best Local Similarity:  96.30%          Conservative:   6
Query Match:            74.07%          Mismatches:     0
DB:                     76.84%          Indels:         1
                                        Gaps:           1

US-09-976-740-20 (1-26) x US-09-517-849-12 (1-1362)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluGluAspAsp---ValSerGluGly 19
          ||||||||||||||||||||||||||||||||||||:::|:|||||||||||||
Db     61 GAGGAGGAGGAGGAGGAGGAAGACGAGGAGGAGGACCACGACGACGACGTCGTTGTTCCGAGGGC 120

Qy     20 SerGluValProGluSerAsp 26
          ||||||||||||||||||||||
Db    121 TCGGAGGTGCCCGAGAGCGAT 141

RESULT 14
US-09-616-289-12
; Sequence 12, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   APPLICANT: Lees, Robert S.
;   APPLICANT: Law, Simon W.
;   APPLICANT: Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;   TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;   TITLE OF INVENTION: ATHEROSCLEROSIS
;   FILE REFERENCE: 10797-004001
;   CURRENT APPLICATION NUMBER: US/09/616,289
;   CURRENT FILING DATE: 2000-07-14
;   PRIOR APPLICATION NUMBER: US 09/517,849
;   PRIOR FILING DATE: 2000-03-02
;   PRIOR APPLICATION NUMBER: US 08/979,608
;   PRIOR FILING DATE: 1997-11-26
;   PRIOR APPLICATION NUMBER: US 60/031,930
;   PRIOR FILING DATE: 1996-11-27
;   PRIOR APPLICATION NUMBER: US 60/048,547
;   PRIOR FILING DATE: 1997-06-03
;   NUMBER OF SEQ ID NOS: 53
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 12
;     LENGTH: 1362
;     TYPE: DNA
;     ORGANISM: Oryctolagus cuniculus
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: (1)...(696)
US-09-616-289-12

Alignment Scores:
Pred. No.:              7.09e-07        Length:         1362
Score:                  104.50          Matches:        20
Percent Similarity:     96.30%          Conservative:   6
Best Local Similarity:  74.07%          Mismatches:     0

---

Score:                  104.50          Matches:        20
Percent Similarity:     96.30%          Conservative:   6
Best Local Similarity:  74.07%          Mismatches:     0
Query Match:            76.84%          Indels:         1
DB:                                     Gaps:           1

US-09-976-740-20 (1-26) x US-09-616-289-12 (1-1362)

Qy      1 GluGluGluGluAspAspAspGluAspGluGluGluAspAsp---ValSerGluGly 19
          ||||||||||||||||||||||||||||||||||||:::|:|||||||||||||
Db     61 GAGGAGGAGGAGGAGGAGGAAGACGAGGAGGAGGACCACGACGACGACGTCGTTGTTCCGAGGGC 120

Qy     20 SerGluValProGluSerAsp 26
          ||||||||||||||||||||||
Db    121 TCGGAGGTGCCCGAGAGCGAT 141

RESULT 15
US-08-979-608A-13
; Sequence 13, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
;   APPLICANT: Lees, Ann M.
;   APPLICANT: Lees, Robert S.
;   APPLICANT: Law, Simon W.
;   APPLICANT: Arjona, Anibal A.
;   TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;                       BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
;                       TREATING ATHEROSCLEROSIS
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/979,608A
;     FILING DATE: 26-No. 6355451-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/048,547
;     FILING DATE: 03-JUN-1997
;     APPLICATION NUMBER: US 60/031,930
;     FILING DATE: 27-NOV-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Myers, Louis
;     REGISTRATION NUMBER: 35,965
;     REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617/542-5070
;     TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1422 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   FEATURE:
;     NAME/KEY: Coding Sequence
;     LOCATION: 1...756
;   SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-979-608A-13

Alignment Scores:
Pred. No.:              7.43e-07        Length:         1422
Score:                  104.50          Matches:        20
Percent Similarity:     96.30%          Conservative:   6
Best Local Similarity:  74.07%          Mismatches:     0

Query Match:          76.84%          Indels:    1
DB:                   4               Gaps:      1

US-09-976-740-20 (1-26) x US-08-979-608A-13 (1-1422)

```
Qy      1 GluGluGluGluAspAspAspGluAspGluGluAspGluAspAsp---ValSerGluGly  19
          |||||||||||:::::::||||||||:::::::||||||        ||||||||||
Db    121 GAGGAGGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGACGTCGTGTCCGAGGGC 180

Qy     20 SerGluValProGluSerAsp  26
          |||||||||||||||||||||
Db    181 TCGGAGGTGCCCGAGAGCGAT 201
```

Search completed: March 13, 2004, 04:06:24
Job time : 10.8152 secs